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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM of: US-09-528-682-1 to: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Command line parameters:
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93:US-09-060-756-48;
93:US-09-172-711-33;
93:US-09-173-711-30:00-10;
94:US-08-1913-00-10;
94:US-08-190-560-1
94:US-08-190-560-1
94:US-08-189-199-1
94:US-08-189-199-1
94:US-08-189-190-560-1
94:US-08-468-946-1
94:US-08-468-946-1
94:US-08-277-1
94:US-08-48-942-1
94:US-08-48-031-13
94:US-08-88-13-88-032-29
94:US-08-88-13-88-22
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q:PCT-US92-03222
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; LOCATION:
US-08-823-120-5
alignment_block:
US-09-528-682-1
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-297-510-42-
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-454-55-5+
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-455-526-42-
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-455-525-42-
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-139-491-42-
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-396-165A-196-
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-295-08-42
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-106-582-42
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-872-644-42
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                                                Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  TELEPHONE: (510) 601-2708
TELEFAX: (510 (655-5542
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/823,120
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VENTUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 4000
CITY: Emeryville
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                   NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 031
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Immunogenic Detoxified Mutants of TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation TITLE OF INVENTION: Their Use for the Preparation of Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                    Quality:
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; Sequence 7, Applicatio
; Patent No. 5874287
                                                alignment_scores:
Quality:
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; MOLECULE TYPE:
US-08-435-605A-7
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            Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,657
REFERENCE/DOCKET NUMBER: A-:
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Burnette, W. Neal
APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINI
TITLE OF INVENTION: SUBUNIT A
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STREET: 1840 De Havilland
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 91320-1789
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                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                          nucleic acid
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                                                                                                                                                                                                           576 base pairs
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              Percent Identity:
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US-09-528-682-1 x US-08-435-605A-7
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                                                                                                                                    Align seg 1/1 to: US-08-435-605A-5
                                                                                                                                                                                                                     Quality: 26.00
Ratio: 1.000
Percent Similarity: 100.000
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ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,657
REFERENCE/DOCKET NUMBER: A-19
REFERENCE/DOCKET NUMBER: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rquence 5, Application:
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 582 base pairs
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 AAGAGGAACTCAGACGGGATTTGTTAGG 162
135 AAGAGGAACTCAGACGGGATTTGTTAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Burnette, W. Neal APPLICANT: Kaslow, Harvey R.
                 45 aArgGlyThrGlnThrGlyPheValArg 54
                                                                    85
                                                                                29 GluTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAl 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 aArgGlyThrGlnThrGlyPheValArg 54
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 0:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/435,605A
FILING DATE: 05-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                  GAGTACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCATGC 134
                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
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1840 De Havilland Drive
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                                                                                                                                                                                                                                                                                                                                                                            single
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57
                                                                                                                                                                                                                       Gaps:
Percent Identity:
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                                                                                                                                      from:
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162
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                                                                                                                                                                                                                                                           Length:
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-823-120-7

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alignment_block:
US-09-528-682-1 x US-08-823-120-7
seq_documentation_block:
; Sequence 1, Application US/08435605A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION:
US-08-823-120-7
                                                          seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-435-605A-1
                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                               Quality: 26.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (510 (655-35)
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Domenighini, Mario
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
TITLE OF INVENTION: Immunogenic Detoxified Mutants of
TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation and
TITLE OF INVENTION: Their Use for the Preparation of Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 11-NOV-1994 ATTORNEY/AGENT INFORMATION: NAME: McClung, Barbara G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                  135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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                                                                                              29 GluTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspH1sAl 45
                                                                                                                                                                           85 GAGTACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCATGC 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: McClung, Barbara
REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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Gaps: 0
Percent Identity: 100.000
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alignment_block:
US-09-528-682-1 x US-08-435-605A-1
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                                                                                                                                                                                                                                                   Sequence 1, Application US/08449045C Patent No. 5770203
                                                                                                                                                                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                         APPLICANT: Burnette, Neal W.
APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                               139 GAGTACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCATGC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 57
                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    189 AAGAGGAACTCAGACGGGATTTGTTAGG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                           45 aArgGlyThrGlnThrGlyPheValArg 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 GluTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAl 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palana
              COUNTRY:
                                      STATE:
                                                                         STREET:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 05-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                           ADDRESSEE:
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                                SSEE: Amgen Inc.
r: 1840 De Havilland Drive
Thousand Oaks
: California
91320-1789
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1840 De Havilland Drive
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                USA
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Gaps:
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alignment_block:
US-09-528-682-1 x 5223610-1
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; LOCATION:
US-08-449-045C-1
                                                                                                        alignment_scores:
                                                                                                                                                                5223610-1
                                                                                                                                                                                                                                                                                                 PATENT NO. 5223610

APPLICANT: Burton, Frank H., Sutcliffe,
TITLE OF INVENTION: CHOLERA TOXIN GENE
                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
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Ratio: 1.000
Percent Similarity: 100.000
                                                    Percent Similarity:
                                                                                                                                                                                                SEQ ID NO:
                                                                                                                                                                                                                                                                                          HORMONE PROMOTER
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7.77 base pairs
                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 02-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
                                                                                                                                                                                                                                                                                                                                                                                                                                    189 AAGAGGAACTCAGACGGGATTTGTTAGG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 GAGTACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCATGC 188
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/694,733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                   FILING DATE: 18-MAY-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                 LENGTH: 2020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                      Quality:
                                                                   Ratio:
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Align seg 1/1

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5223610-1

from:

to: 2020

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REFERENCE/DOCKET NUMBER: 18,872;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9909
TELEFAX: (212) 869-8864/9741
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 hass miles
                                                                                                                                                                                           alignment_block:
US-09-528-682-1 x US-08-296-848A-1
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seq_documentation_block:
                                    seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-435-605A-9
                                                                                                                                                                                                                                                                                                                                                                          US-08-296-848A-1
                                                                                                                                                                                                                                                    Quality: 15.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                        Align seg 1/1 to: US-08-296-848A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
NOBITCONTINUED: 15 /08 /06 6446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 GlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn 200
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                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Clements, John D.
APPLICANT: Dickinson, Bonny L.
TITLE OF INVENTION: MUTANT ENTEROTOXIN EFFECTIVE AS
TITLE OF INVENTION: NON-TOXIC ORAL ADJUVANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 aArgGlyThrGlnThrGlyPheValArg 54
                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: doul TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 26-AUG-1994 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 45 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGAGGAACTCAGACGGGATTTGTTAGG 731
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                                                                                                                                                                                                                                                      Percent Identity:
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alignment_block: US-09-528-682-1 \times US-08-435-605A-9
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Percent Similarity:
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Sequence 23, Application US/08449045C
Patent No. 5770203
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Burnet
APPLICANT: Kaslow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                         APPLICANT: Burnette, Neal W. APPLICANT: Kaslow, Harvey R. TITLE OF INVENTION: SUBUNIT ANALOGS NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: Callfornia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 GluTyrGlnSerLysValLysArgGlnIlePheSer 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                   55 GAATACCAATCTAAAGTTAAAAGACAAATATTTTCA 90
                                                                COUNTRY: USA
ZIP: 91320-1789
                                                                                                  CITY: Thousand Oaks
STATE: California
                                                                                                                                         STREET:
                                                                                                                                                             ADDRESSEE:
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                                                                                                                                   E: Amgen Inc.
1840 De Havilland Drive
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1840 De Havilland Drive
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IVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
IVENTION: SUBUNIT ANALOGS
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Gaps: 0
Percent Identity: 100.000
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alignment_scores:
    Quality:
    Ratio:
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)8-449-045C-23
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 07/694,733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
                                      PRIOR APPLICATION DATA:
                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Burnette, Neal W.
APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 TrpIleHisHisAlaProGlnGlyCysGlyAsn 189
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                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: RECOMBINANT DNA TITLE OF INVENTION: SUBUNIT ANALOGS
                                                                                                                    APPLICATION NUMBER: FILING DATE: 24-MAY CLASSIFICATION: 424
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                                                         APPLICATION NUMBER: US 07/694,733 FILING DATE: 02-MAY-1991
                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Amgen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                APPLICATION NUMBER:
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MBER: US 08/271,222
06-JUL-1994
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1.000
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alignment_block:
US-09-528-682-1 x US-08-449-045C-24
US-08-435-605A-35
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                        APPLICATION NUMBER: US/08/
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAZZA, Richard J.
REGISTRATION NUMBER: 27,65
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-449-045C-24 from: 1 to:
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Patent No. 5
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              TOPOLOGY: 11
MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Burnette, W. Neal APPLICANT: Kaslow, Harvey R. TITLE OF INVENTION: RECOMBINIT ATTILE OF INVENTION: SUBUNIT A
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LENGTH: 50 base pairs
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                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Thousand Oaks
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1840 De Havilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                          linear
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              other nucleic acid
/desc = "oligonucle
                                                                          single
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57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RECOMBINANT DNA-DERIVED CHOLERA TOXIN
                                                                                                                                                                                                                                                                                                     US/08/435,605A
                  "oligonucleotide"
                                                                                                                                                            35:
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alignment_scores:

Quality: Ratio:

11 0

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seq_documentation_block:
; Sequence 14, Application US/08629600
; Patent No. 5783196
                                                                                                                                                                                                                                                alignment_block:
US-09-528-682-1 x US-08-435-605A-36
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; Sequence 36, Applicati
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US-09-528-682-1 x US-08-435-605A-35
                                                                                           seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-629-600-14
                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
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Percent Similarity:
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GENERAL INFORMATION:
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: A INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
                                                                                                                                                        179 TrpIleHisHisAlaProGlnGlyCysGlyAsn 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,605A
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 TrpIleHisHisAlaProGlnGlyCysGlyAsn 189
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN TITLE OF INVENTION: SUBUNIT ANALOGS NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Burnette, W. Neal APPLICANT: Kaslow, Harvey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1840 De Havilland Drive CITY: Thousand Oaks
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                                                                                                                                    TGGATTCATCATGCACCGCAGGGTTGTGGGAAT 35
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5874287
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/desc = "oligonucleotide"
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; MOLECULE TYPE:
; HYPOTHETICAL:
US-08-629-600-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                 Sequence 36,
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 293-781 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/629,600
FILING DATE: 9-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
                                                                                                                                       TITLE OF INVENTION: Immunogenic Detoxified Mutants of TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their TITLE OF INVENTION: Their Use for the Preparation of Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GUA MUTANTS OF SHIGELLA TITLE OF INVENTION: AND VACCINES CONTAINING THE SAME NUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS:
                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                           APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
                                                                                                                                                                                                                                                                                                                                                                                                           192 ArgThrIleThrGlyAspThrCysAsnGlu 201
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MEDIUM TYPE: Floppy disk
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                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                            13
                                   STATE:
                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
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                                                  STREET: 4560 Horton Street CITY: Emeryville
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                COUNTRY:
                                                                                     ADDRESSEE:
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94608-2916
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                                 California
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                                                                                                                                                                                                                              Domenighini, Mario
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LEVINE, Myron M.
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E: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                       Chiron Corporation
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TOPOLOGY: 11; MOLECULE TYPE: US-08-823-120-36
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US-09-528-682-1 x US-08-823-120-36
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Quality:
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Ratio: 1.000
Percent Similarity: 100.000
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Patent No. 5631010
GENERAL INFORMATION:
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                                  FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION NUMBER: US/08/403,584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0315.001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,003
FILING DATE: 11-NOV-1994
                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mekalanos, John J.
TITLE OF INVENTION: DELETION MUTANTS AS VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/823,120
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                                                                                                                                                                                                                                                        COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                   CITY: Boston
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                              STATE: Massachusetts
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(510) 655-3542
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US/07/909,382
                                        US/08/083,388
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Percent Identity: 100.000
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alignment_block: us-09-528-682-1 \times us-08-367-115-5
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Quality:
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; ORGANISM: Vibrio cholerae
US-08-367-115-5
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US-09-528-682-1 x US-08-403-584-5
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Ratio: 1.000
Percent Similarity: 100.000
                                                                       Align seg 1/1 to:
                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID: NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08367115 Patent No. 5874088
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                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/08/367,115
CURRENT FILING DATE: 1995-01-05
EARLIER APPLICATION NUMBER: CT/US93/06270
EARLIER FILING DATE: 1993-07-01
EARLIER APPLICATION NUMBER: 07/909,382
EARLIER FILING DATE: 1992-07-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 0074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mekalanos, John J.
APPLICANT: Beattie, David
APPLICANT: Killeen, Kevin
APPLICANT: Lu, Yichen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: DELETION MUTANTS AS VACCINES FOR CHOLERA FILE REFERENCE: 00742/002002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                             LENGTH: 32
                 217 LysValLysArgGlnIlePheSer 224
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6 AAAGTTAAAAGACAAATATTTTCA 29
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alignment_block:
US-09-528-682-1 x PCT-US93-06270-5
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                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-296-848A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: PCT-US93-06270-5
                                                                                                                                                                       Sequence 4, Application US/08296848A Patent No. 6019982 GENERAL INFORMATION:
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                          NAME: Freeman, John W.
REGISTION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5970
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                    APPLICANT: Clements, John D.
APPLICANT: Dickinson, Bonny L.
TITLE OF INVENTION: MUTANT ENTEROTOXIN EFFECTIVE AS
TITLE OF INVENTION: NON-TOXIC ORAL ADJUVANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06270
FILING DATE: 19930701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mekalanos, John J.
TITLE OF INVENTION: DELETION MUTANTS AS VACCINES FOR
TITLE OF INVENTION: CHOLERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Freeman, John W.
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ADDRESSEE: Fish & Richardson
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Gaps: 0
Percent Identity: 100.000
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alignment_scores:
Quality:
                                                                                                                                             ; SEQ ID NO 1
LENGTH: 31491
; TYPE: DNA
; ORGANISM: Capsicum annuum
US-09-360-186-1
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US-09-528-682-1 x US-08-296-848A-4
alignment_block:
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                               Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Staskawicz,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09360186 Patent No. 6262343
                                                                                                                                                                                                                                                       CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: 60/093,957
EARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/360,186
CURRENT FILING DATE: 1999-07-23
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NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 5113

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Bs2 Resistance Gene FILE REFERENCE: 50687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,848A
FILING DATE: 26-AUG-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 ThrileThrGlyAspThrCysAsn 200
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LENGTH: 45 base pairs
TYPE: nucleic acid
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MOLECULE TYPE:
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STATE:
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(212) 869-8864/9741
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                               Length: 8
Gaps: 0
Percent Identity: 100.000
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Percent Identity: 100.000
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-07-932-379A-11
                                  alignment_scores:
Quality:
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 Ratio: 1.000
Percent Similarity: 100.000
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Stewart, Raymond C.
REGISTRATION NUMBER: 21,066
REFERENCE/DOCKET NUMBER: 1327
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL
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ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 N. Washington St.
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yamagata, Koichi
TITLE OF INVENTION: Oligonuclectides for Detecting
TITLE OF INVENTION: Bacteria and Detection Method
TITLE OF INVENTION: Using Same
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                             HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: UPFILING DATE: 19920819 CLASSIFICATION: 435
                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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ZIP: 22046-3487
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Fukushima, Shigeru
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Shirasaki, Yoshinari
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/note= "Identification method S"
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Length: 7
Gaps: 0
Percent Identity: 100.000
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-932-379A-12
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alignment_scores:
                                                         ; OTHER INFORMATION: ; OTHER INFORMATION: US-07-932-379A-12
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FILING DATE: 1920819
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Stewart, Raymond C.
REGISTRATION NUMBER: 21,066
REFERENCE/DOCKET NUMBER: 1327
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEFAX: 703-241-2848
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                                                                                                                                                                                         MOLECULE TYPE: D
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nishimura, Nasyuki
APPLICANT: Shirasaki, Yoshinari
APPLICANT: Yamagata, Koichi
TITLE OF INVENTION: Oligonuclectides for Detecting
TITLE OF INVENTION: Bacteria and Detection Method
TITLE OF INVENTION: Using Same
                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 7248345
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                                                                                                                 NAME/KEY:
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STREET: 301 N. Washington St.
CITY: Falls Church
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                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
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ZIP: 22046-3487
                                                                                                                                                                                                                                                                                                           NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toda,
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                                                                                                                 1..22
                                                                                                                                                                           Eschericia coli H10407
                                                                                                                                                                                                                                                                         linear
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                                                                         /label= oligonucleotide
/note= "Identification method
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Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000

Length: 7
Gaps: 0
Percent Identity: 100.000

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; NAME/KEY: 1..22; LOCATION: 1..22; OTHER INFORMATION: ; OTHER INFORMATION: ; OTHER INFORMATION: ; OTHER INFORMATION: US-08-379-295-11
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US-09-528-682-1 x US-07-932-379A-12/rev
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TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICATION NUMBER: US/07/932,379A
FILING DATE: 19-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC computable
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Birch, Stewart, Ko
ADDRESSEE: 301 N. Washington St.
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Oligonucleotides for Detecting TITLE OF INVENTION: Bacteria and Detection Method TITLE OF INVENTION: Using Same
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                                                                                           FEATURE:
                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                               HYPOTHETICAL:
ANTI-SENSE: NO
                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Nishimura, Nasyuki
APPLICANT: Shirasaki, Yoshinari
APPLICANT: Yamagata, Koichi
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                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 21,066
REFERENCE/DOCKET NUMBER: 13:
                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                        TOPOLOGY:
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5516898
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Fukushima, Shigeru
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                                                                                                            Eschericia coli H10407
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                 /label= oligonucleotide
/note= "Identification method
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alignment_block:
US-09-528-682-1 x US-08-379-295-11
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                                                                                                                                                                                                                                     TELEX: 248345
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/932,379A
FILING DATE: 19-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Raymond C:
                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
                                                                                                                                                                               SEQUENCE CHARACTERISTICS
LENGTH: 22 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT:
                                                                                   ORIGINAL SOURCE:
                                                                                                 MOLECUE PARTICAL: PROTHETICAL: PROTHETICAL: NO
                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA
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                                                   FEATURE:
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CITY: Falls Church
STATE: Virginia
LOCATION: 1..22
OTHER INFORMATION:
                                                                                                                                                                                                                                                TELEFAX: 705 A
                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                   NAME: Stewart, 21,066
REGISTRATION NUMBER: 21,066
1327-106P
                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                               STRANDEDNESS: single
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                               NAME/KEY:
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Shirasaki, Yoshinari
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Fukushima, Shigeru
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                                                                   Eschericia coli H10407
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Bacteria and Detection Method
/label- oligonucleotide
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; OTHER INFORMATION: US-08-379-295-12
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US-09-528-682-1 x US-08-379-295-12/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
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                                                                                                                                                                                                               TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                    HYPOTHETICAL: N
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 SerGluValAspIleTyrAsn 234
                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/932,379
FILING DATE: 19-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yamagata, Koichi
TITLE OF INVENTION: Oligonucleotides for Detecting Bacteria
TITLE OF INVENTION: and Detection Method Using Same
                    FEATURE:
                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Toda, Jum
APPLICANT: Fukushima, Shigeru
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                                                                                                                                                                                                                                                                                                         NAME: Weiner, Marc S. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/379,296 FILING DATE: 27-JAN-1995
   NAME/KEY:
                                     ORGANISM:
                                                                                                                              TOPOLOGY:
                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
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                                                                                                                                                                                LENGTH:
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T: P.O. Box 747
Falls Church
                                                                                                                                                              nucleic acid
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Shirasaki, Yoshinari
                                     Eschericia coli H10407
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Gaps: 0
Percent Identity: 100.000
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-379-296-11
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US-09-528-682-1 x US-08-379-296-11
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                                                                                                                                                                                TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
                                     MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                 NAME: Weiner, Marc S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                    FILING DATE: 19-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weiner, Marc 9
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08
FILING DATE: 27-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Oligonucleotides for Detecting Bacteria TITLE OF INVENTION: and Detection Method Using Same NUMBER OF SEQUENCES: 53
                                   ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                               TELEPHONE: 703-205-8050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Birch, St
STREET: P.O. Box 747
CITY: Falls Church
ORGANISM:
                                                                                          TOPOLOGY:
                                                                                                       STRANDEDNESS:
                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22040-0747
                  SOURCE:
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Shirasaki, Yoshinari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ozaki, Hiroko
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                                                                                      linear
Eschericia coli H10407
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O
                                                                         DNA
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/note= "Identification method S"
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STRANDEDNESS: sinc
TOPOLOGY: linear
MOLECULE TYPE: DNA (
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Vibrio (
US-08-328-710A-26
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US-09-528-682-1 x US-08-379-296-12/rev
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Ratio: 1.000
Percent Similarity: 100.000
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Patent No. 5
                                                                                                                                                                                       TELEFAX: (703) 205-805
TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Weiner, Marc S
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 105-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Nakaya
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                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: U$/08/328,710A FILING DATE: 25-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Oligonuclectides TITLE OF INVENTION: PICCESS NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                        CENGTH:
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ET: PO Box 747
: Falls Church
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5795717
                                                                                                                                                    nucleic acid
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                                                                                                                                                                        22 base pairs
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                     Vibrio cholerae
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                                                                                             DNA (genomic)
                                                                                                                                  single
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Gaps: 0
Percent Identity: 100.000
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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
                                                                                                  ; HYPOTHETICAL: no ; ANTI-SENSE: yes ; FRAGMENT TYPE: US-09-311-260-134
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US-09-528-682-1 x US-08-328-710A-26/rev
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   Quality:
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                               NAME: Larson, Marina T.
REGISTION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word Perfect CURRENT APPLICATION DATA:
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ADDRESSEE: Oppedahl & Larson LLP
STREET: P.O. Box 5270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LACTOIX, Jean-Michel TITLE OF INVENTION: METHOD, COMTITLE OF INVENTION: MICROGRANITITLE OF INVENTION: POLYMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: li
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LENGTH: 22
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MEDIUM TYPE: Diskette -
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                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                TELEFAX: (970) 668-2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
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100.000
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                                                                                                                   internal
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Length:
Gaps:
Percent Identity:
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Percent Identity:
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alignment_block:
US-09-528-682-1 x US-08-968-046-26/rev
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US-09-528-682-1 x US-09-311-260-134
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                                                                                                                                                                                         US-08-968-046-26
                                                                                 Ratio:
Percent Similarity:
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Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 205-805
TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                       HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Vibr
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ohashi, Tetsuo
TITLE OF INVENTION: Oligonucleotides for detecting bacteria
TITLE OF INVENTION: and detection process
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 00
FILING DATE: 25-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: PO Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgAlaAspSerArgProPro 13
                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                       nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weiner, Marc S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08968046
to reverse of: US-08-968-046-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PO Box 747
                                                                                                                                                                                                                                                                                                                                                                                                           (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukushima, Shigeru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakayama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                         Vibrio cholerae
                                                                                                                                                                                                                                                                                         linear
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                                                                                 : 7.00
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                                                                                                                                                                                                                                                                                                         single
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                                                                                 Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1422-202P
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: 0
: 100.000
 from: 1
to: 22
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alignment_block:
US-09-528-682-1 x US-08-363-585-12
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                                                                                                     alignment_scores:
                                                                                                                                                       US-08-363-585-12
                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 27 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/07/786,228
APPLICATION NUMBER: US/07/786,228
APPLICATION NUMBER: US/07/786,228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Frederick H. Colen; Mary-Elizabeth Buckles
REGISTRATION UNMBER: 28,061; 31,907
REFERENCE/DOCKET NUMBER: 92-232
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 SerGlnIleTyrGlyTrpTyr 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 5-1/4" low density diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                         PUBLICATION INFORMATION:
AUTHORS: Rudert, W.A.
                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: University of Pittsburgh STREET: Office of Intellectual Property STREET: 911 William Pitt Union
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC or compatibles
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
                                                                                                                                                                                     PAGES: 352-356
DATE: 1992
                                                                                                                                                                                                                                                         TITLE: A NO. 5683872el Approach to Rapid HLA Class TITLE: Molecular Typing
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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TELEFAX: 412/288-3063
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                                                                                                                                                                         RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                            AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-363-585-12
                                                                                     Quality:
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5683872
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                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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As The Bound Ligands For Use In Re
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                                                   Length:
Gaps:
Percent Identity:
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                                                   100.000
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Align seg 1/1 to: US-08-363-585-12

from:

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seq_documentation_block:

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-142-355B-11

ArgSerGlyGlyLeuMetPro

25 4

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seq_documentation_block:
; Sequence 65, Applicati
; Patent No. 5646029
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US-09-528-682-1 x US-09-142-355B-11/rev
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Quality:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows
SEQ ID NO 11
LENCTH: 42
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/GB97/01153
PRIOR FILING DATE: 1997-04-25
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/142,355B
CURRENT FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: GB 9608540.2
PRIOR FILING DATE: 1996-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tawfik, Dan. S.
APPLICANT: Winter, Gregory Paul
TITLE OF INVENTION: Isolation of Enzymes
FILE REFERENCE: 2224/0E665
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                              APPLICANT: (
APPLICANT: (
APPLICANT: (
APPLICANT: (
                                                                                                                                                     NUMBER OF SEQUENCES: 9:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         APPLICANT: Clarke, Adrienne E
TITLE OF INVENTION: Plant Arabinogalactan Protein (AGP) Genes
                                                                              STREET: J..
STREET: J..
STREET: J..
STREET: J..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 AGTACCAGCCTCAGCCTGCGG 15
                                                           COUNTRY: United States of America
                                                                                                                                     ADDRESSEE:
                                           80303
                                                                                                                                                                                                                                                                                                                                              5, Application US/08276452A 5646029
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                                                                          Colorado
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Viti, Francesca
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                                                                                                                  E: Greenlee and Winner, P.C. 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                     Chen,
                                                                                                                                                                                                                            Gane, Alison M
Bacic, Antony
                                                                                                                                                                                                                                                                                       Mau,
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Shaio-Lim
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Gaps: 0
Percent Identity: 100.000
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seq_documentation_block:
; Sequence 65, Application US/08798744
; Patent No. 5830747
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                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-798-744-65
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Chen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (303)499-808
TELEX: 49617824
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/276 ***
FILING DATE: 18-,THT-1^*
CLASSTETO^*:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 85 base pairs
                                                                                    STREET: Soulder CITY: Boulder Colorado united
                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   APPLICANT: Clarke, Adrienne E
TITLE OF INVENTION: Plant Arabinogalactan Protein (AGP) Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 LeuArgGluTyrGlnSerLys 217
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                                                                                                                                                                                                                                                                              APPLICANT:
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OTHER INFORMATION: /not
OTHER INFORMATION: to r
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OTHER INFORMATION: /no:
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STRANDEDNESS: single
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 OPERATING SYSTEM:
                                                                                                                                              ADDRESSEE: Greenlee and Winner, P.C. STREET: 5370 Manhattan Circle, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGCGGGAGTATCAGTCAAAA 84
                                                                       80303
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Mau, Shaio-Lim
                                                                                                                                                                                                                                                         Gane, Alison M
Bacic, Antony
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                                                                                                                                                                                                                                                                                               Du, He
                                                                                        United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                Chao-Guang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Adaptor sequence is equal
to nucleotides 444-461 of the NaAGP1 cDNA"
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                                                                                          of America
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CURRENT APPLICATION DATA:

PatentIn Release #1.0, Version #1.25

CLASSIFICATION: 435 APPLICATION NUMBER: FILING DATE: 13-FE

13-FEB-1997

US/08/798,744

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alignment_block:
US-09-528-682-1 x US-08-798-744-65
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Quality:
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-798-744-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-060-756-266
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                    CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 266
                                                                                                                                                                                                               APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gordon, Stephen
APPLICANT: Biliault, Alain
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169
                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                              LENGTH: 21
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 49617824
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    equence 266,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        documentation_block:
FEATURE:
NAME/KEY: unsure
                                     ORGANISM: Mycobacterium tuberculosis
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TELECOMMUNICATION INFORMATION:
TELLEPHONE: (303)499-8080
TELEFAX: (303)499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Caruthers, Jennie M
REGISTRATION NUMBER: 34,44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: 68..85
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6183957
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to nucleotides 444-461 of the NaAGP1 cDNA"
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Gaps: 0
Percent Identity: 100.000
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alignment_scores:
    Quality:
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alignment_scores:
Quality:
Ratio:
                                                                                              ; TOPOLOGY: 1; MOLECULE TYPE: US-08-471-780C-95
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION NATA:
APPLICATION UMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
                                                                                                                                                                                                                                                                      TELEPHONE: 202-408-4000
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APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglo
NUMBER OF SEQUENCES: 130
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                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                NAME: Potter, Jane E.R. REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 06-JUN
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                                                                                                                                                                                              LENGTH:
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nucleic acid
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alignment_block:
US-09-528-682-1 x US-08-467-282B-95/rev
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; Patent No. 5800988
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US-09-528-682-1 x US-08-471-780C-95/rev
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Ratio: 1.000
Percent Similarity: 100.000
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                                     Align seg 1/1 to reverse of: US-08-467-282B-95
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC LOSS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,282B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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TOPOLOGY: lin
MOLECULE TYPE:
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62 ThrSerLeuSerLeuArgSer 68
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1300 I Street, N.W.
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Gaps:
Percent Identity:
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seq_documentation_block:
; Sequence 95, Application US/08466710C
; Patent No. 5874541
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                                                                            seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-466-710C-95
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INFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,282A
FILING DATE: 06-JUN-1995
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MEDIUM TYPE: Floppy disk
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LENGTH: 433 base pairs
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                                                                                                                                                       62 ThrSerLeuSerLeuArgSer 68
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CITY: Washington
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Ratio:
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21-AUG-1992
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                                                                                                                                                                                                                                                                                     Gaps:
Percent Identity:
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                                                                                                                                                                                                                                                                                     100.000
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GENERAL INFORMATION:

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to reverse of: US-08-466-710C-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                          Sequence 95, Application US/08471284B Patent No. 6005079
                                                     GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunogle
NUMBER OF SEQUENCES: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                   09-528-682-1 x US-08-466-710C-95/rev
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                340 ACGTCCTTGTCGCTAAGGTCG
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                                       CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: FR 9:
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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APPLICANT: Hamers, Raymond
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                                                                                                                                                                                                                                                                                                                       62 ThrSerLeuSerLeuArgSer 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                      ADDRESSEE:
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Finnegan, Henderson, Farabow, Garrett & Dunner
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21-MAY-1993
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                                                         Immunoglobulins Devoid of Light Chains 130
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-468-739C-95
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US-09-528-682-1 x US-08-471-284B-95/rev
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Quality:
Ratio:
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                     Sequence 95,
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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ATTORNEY/AGENT INFORMATION:
NAME: POLLET, Jane E.R.
REGISTRATION NUMBER: 33,:
REFERENCE/DOCKET NUMBER:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,284B
                                                                                                                                                                                                                         APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: FR 92
TTNG DATE: 21-AUG-1992
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CITY: Washington
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FILING DATE: 17-AUG-1993
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                                                                                                                   STATE:
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                                                                                              COUNTRY:
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                                                                                                                                                                     ADDRESSEE:
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alignment_block:
US-09-528-682-1 x US-08-468-739C-95/rev
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No. 5759808
ENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 08/106,944
APPLICATION NUMBER: 17-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-471-780C-96
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FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                    CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
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                                                                            APPLICATION NUMBER: US/0 FILING DATE: 06-JUN-1995
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APPLICATION NUMBER: US 08/106,944 FILING DATE: 17-AUG-1993
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20005-3315
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1300 I Street, N.W.
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Percent Identity: 100.000
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-471-780C-96
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 96,
                                                                                                                                                                                                                                                                    ZIP: 2005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release.
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LENGTH: 449 base pairs
TYPE: nucleic acid
                                                                                        APPLICATION NUMBER: FR 9
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                     APPLICATION NUMBER: FR 93401310.3 FILING DATE: 21-MAY-1993 ATTORNEY/AGENT INFORMATION: NAME: Potter, Jane E.R.
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                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/467, 282B FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
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NAME: Potter, Jane REGISTRATION NUMBER:
                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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1300 I Street, N.W.
                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
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                                                                                                                               FR 92402326.0
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Percent Identity:
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-471-282A-96
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Ratio: 1.000
Percent Similarity: 100.000
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Sequence 96, Applicati
          TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                         REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
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                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 06-JUN
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LENGTH:
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1300 I Street, N.W.
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; STRANDEDNESS:
; TOPOLOGY: lin
; MOLECULE TYPE:
US-08-471-282A-96
; TOPOLOGY: 1; MOLECULE TYPE: US-08-466-710C-96
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    Quality:
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Percent Similarity: 100.000
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                                                                                                                                                                                                                             FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 934.
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: POTTER, Jane E.R.
REGISTRATION NUMBER: 33,33;
                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 449 base pairs
TYPE: nucleic acid
                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
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APPLICANT:
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                                                      STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: UFILING DATE: 17-AUG-1
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                                                                                                                                                                                                                   04958.0008-00000
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alignment_scores:
 Quality:

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alignment_block:
US-09-528-682-1 x US-08-471-284B-96/rev
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US-09-528-682-1 x US-08-466-710C-96/rev
                                                                                                                                                                                                               ; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-471-284B-96
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                                                                                            Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
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Align seg 1/1
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Casterman, Cecil
APPLICANT: Hamers, Raymond
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APPLICATION NUMBER: US/08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                      RECISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
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ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
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CITY: Washington
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                                                                                                                                                                                                                                                                                                           LENGTH:
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to reverse of: US-08-471-284B-96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Finnegan, Henderson, Farabow, Garrett & Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: FR 93401310.3
21-MAY-1993
                                                                                                                                                                                                                                                                     single
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Percent Identity:
                                                                                            Percent Identity:
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                                                                                                                                  Length:
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from: 1
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seq_documentation_block:
; Sequence 17, Application US/08050259B
                                                      seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-050-259B-17
                                                                                                                                                                                                         alignment_block:
US-09-528-682-1 x US-08-468-739C-96/rev
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                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                              US-08-468-739C-96
                                                                                                                                                                                                                                                         Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/ACENT INFORMATION:
NAME: POLLEY, Jane E.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Casterman, Cecile APPLICANT: Hamers, Raymond TITLE OF INVENTION: Immunoglo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                              62 ThrSerLeuSerLeuArgSer 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 ThrSerLeuSerLeuArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US C. APPLICATION NUMBER: US C. APPLICATION NUMBER: FR 92402326.0
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                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Potter, Jane E.R. REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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SYSTEM: PC-DOS/MS-DOS
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seq_documentation_block:
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Ratio: 1.000
Percent Similarity: 100.000
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Patent No. 5907085
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                                                                                                                                            GENERAL INFORMATION:
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
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09-528-682-1 x US-08-050-259B-17/rev
                                    APPLICANT: Gonsalves, Dennis
APPLICANT: Ling, Kai-Shu
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND
TITLE OF INVENTION: THEIR USES
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,259B
                                                                                                                                                                                                                                                                                            446 GGCTACAGGCTGGCTTC
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REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/GB91/01898
FILLING DATE: 30-CCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9023907.0
FILING DATE: 02-NOV-1990
ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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                       CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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APPLICANT: Valerie Wells
TITLE OF INVENTION: CELL GROWTH INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                     161 GlyTyrArgLeuAlaGlyPhe 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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CITY: San Francisco
STATE: CA
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    ADDRESSEE:
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Dreger, Walter H.
NIMBER: 24,190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             497 bases
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                     ADDRESS:
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N: 530
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Hargrave, Devans & Doyle LLP
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                                                                                                                                                                                                                                                                                            426
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-133-804-3
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08133804 Patent No. 5534254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 21-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: GOldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 1960
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                            APPLICANT: Oppermann, Hermann APPLICANT: Houston, L. L. APPLICANT: Ring, David B. TITLE OF INVENTION: Biosynthematic of Invention: Imaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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                                                                                                     COUNTRY:
                                                                                                                        STATE:
                                                                                                                                       CITY: Boston
                                                                                                                                                         STREET:
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CITY: Rochester
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Y: U.S.A.
                                                                                                                       Massachusetts
                                                                                                                                                     Exchange Place,
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CURRENT APPLICATION DATA: APPLICATION NUMBER: US,

US/08/133,804

FILING DATE:

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APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Blosynthetic Binding Proteins For INUBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa
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Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
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US-09-528-682-1 x US-08-133-804-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-461-838-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7100
TELEPAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-133-804-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08461838 Patent No. 5753204
APPLICATION NUMBER: US/08/461,838 FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION UNMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                729 GAGATTAAACGTTCCGGGGGA 749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 3..758
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 GluIleLysArgSerGlyGly 21
                                                                                                                                                                                                                                                                       STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                       02109
                                                                                                                                                                                                                                                                                                                Boston
                                                                                                                                                                                                                                                                                                                            E: Testa, Hurwitz & Thibeault/Patent Department Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "26-10 sFv' with C-terminal Gly4-Cys"
                                                                                                                US/08/461,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Gaps:
Percent Identity:
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                                                                                                                                                         Version #1.
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; NAME/KEY: CDS
; LOCATION: 3..758
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-461-838-3
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US-09-528-682-1 x US-08-461-838-3
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Quality:
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Ratio: 1.000
Percent Similarity: 100.000
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TELEPHONE: 617-248-7477
TELEPAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 779 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
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Percent Identity: 100.000
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REFERENCE/DOCKET NUMBER: A-
REFERENCE/DOCKET NUMBER: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
TYPE: nucleic acid
TYPE: nucleic single
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Ratio: 1.000
rcent Similarity: 100.000
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                                                                                                                                                                                                                                                          .g_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-449-045C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gnment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
R: IBM PC compatible
COMPAN NG SYSTEM: PC-DOS/MS-DOS
OPEL NG SYSTEM: PRO-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPPLICANT: BUTNETTE, W. NEWL
PPLICANT: Kaslow, Harvey R.
ITTLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
FITLE OF INVENTION: SUBUNIT ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     int No. 5874287
TERAL INFORMATION:
                                                                                                                                                                                             Sequence 1, Application US/08449045C Patent No. 5770203
                                                                                                                                                                                                                             g_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,657
                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Amgen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
                                                                                      APPLICANT: BUTNETTE, Neal W. APPLICANT: BUTNETON: HECOMBINAN TITLE OF INVENTION: SUBUNIT AN NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/435,605A
STATE: C
COUNTRY:
ZIP: 913
                       STREET: 1040 CITY: Thousand Oaks
STATE: California
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                                                                            DDRESSEE:
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   RY: USA
91320-1789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.30
                                                              E: Amgen Inc.
1840 De Havilland Drive
                                                                                                                            RECOMBINANT DNA-DERIVED CHOLERA TOXIN SUBUNIT ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 Gaps: 0 percent identity: 100.000
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; LOCATION:
US-08-449-045C-1
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US-09-528-682-1 x US-08-449-045C-1
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APPLICATION NUMBER: US 07/694,733
APPLICATION NUMBER: US 08/271,222
APPLICATION NUMBER: US 08/271,222
APPLICATION NUMBER: US 08/271,222
ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,657
REGISTRATION NUMBER: 27,657
                                                                                                                                                                                                                                                    seq_documentation_block:
;patent No. 5223610
APPLICANT: Burton, Frank H.;Sutcliffe, Gregor
TITLE OF INVENTION: CHOLERA TOXIN GENE REGULATED BY GROWTH;
                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5223610-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   percent similarity: 100.000
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alignment_block:
US-09-528-682-1 x 5223610-1
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                    Quality: 26.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                              SEQ ID NO:1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 777 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/449,045C FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE: 18-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                  LENGTH: 2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
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percent Identity: 100.000
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                                                    Percent Identity:
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9b_ph:AE004224
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9b_ba:ECOETTOXHL
9b_ba:ECOETTOXHL
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9b_ba:AF452584

9b_ba:AF463401

9b_ba:VIBCTXABA

9b_pat:A16422

9b_pat:A16422

9b_pat:E00132

9b_pat:E00132

9b_ba:VCTOXAB1

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gb_ba:ECOTOXA
gb_ba:S60731
gb_ba:S60731
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gb_ba:P307LTA
gb_pat:A04913
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Database sequences: 1797656
Database length: 1873333701
Search time (sec): 3690.420000
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Query: US-09-528-682-1
Query length: 240
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gb_pat:AR118597
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Sequence
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-GAPOP=6.000 -GAPEXT=7.000 -XARPOP=10.000 -YARPEXT=0.500
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-DELOCAL -OUTFMT=10 - HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -NO_XLPXY -WAIT -THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of: US-09-528-682-1 to: GenEmbl:*
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                     1885.
1876.
1630.
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1178.
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588.
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.0e-117
.8e-107
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       9b_htg:AL455318
9b_pr:AP001660
9b_ba:AF1177946
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gb_ba:BPETOX
gb_pat:B01352
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gb_pr:HSDJ92C8
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9b_ba:MITV016
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gb_htg:AC024537
gb_in:AF078796
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gb_ba: AE009027
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gb_pat:I03425
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596 | AE007993 Agrobacterium tum
197 | AE009027 Agrobacterium tum
5570 | AL160451 Homo sapiens chr
0000 | Continuation (2 of 4) of
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9300 | AL590076 Human DNA sequen
4926 | AP001347 Homo sapiens gen
3833 | AL450318 Homo sapiens gen
25 | AF177946 Streptomyces coeli
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27 | Al35989 Streptomyces coeli
01 | AJ245368 Bordetella pertussi
16 | X16347 Bordetella pertussi
17 | AF00483 Brevibacilius bre
18 | AC094866 Rattus norvegicu
18 | X16347 Zea mays beta-p-gluc
19 | X16347 Zea mays strain
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10 | AL157916 Streptomyces coerev
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10 | AL646077 Ralstonia solana
10 | AL167916 Dordetella pertussi
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11 | AV058092 Sequence 11 from
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751 | AC107423 Homo sapiens chr
963 | AC024537 Homo sapiens chr
4 | AF078796 Caenorhabditis ele
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4 I AE001886 Deinococcus radio
4 I AE009105 Agrobacterium tum
7 I AE008070 Agrobacterium tum
8 I AE009114 Nycobacterium tum
9 I AL590443 chromosome III o
1 AB030315 Pieris rapae mRNA
1 E51095 Apoptosis-Inducing per
1 AJ245366 Bordetella pertussi
1 AJ06155 Bordetella pertussi
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1 AJ006158 Bordetella pertussi
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1 AJ006157 Bordetella pertussi
1 AJ007364 Bordetella pertussi
1 AJ007365 Bordetella pertussi
1 AJ00736 Pieris brassicae m
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1 M1378 Bordetella pertussis
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| AL132671 Human DNA Sequen
| 0 | AL646079 Ralstonia solana
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M61015 Escherichia coli heat
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+ 82.00 108.34	+ 82.00 120.51	+ 82.00 120.34	+ 82 00 120 94	+ 82 00 123 80	+ 82.00 124.14	+ 82.00 124.92	+ 82.00 129.11	+ 82.00 131.97	+ 82.00 132.33	+ 82.00 132.37	+ 82.00 I33.21	+ 82.00 134.02	+ 62.00 134.08	62.00 70.02	. 03 50 75 03	- 82.50 76.23	+ 82.50 76.35	+ 82.50 77.09	- 82.50 77.57	- 82.50 //.8/	00.00	- 82 50 79 49	- 82.50 81.65	4 82.50 82.16	00000	+ 82.50 82.18	+ 82.50 82.57	- 82.50 65.04	1 00 50 05 0A	- 82.50 93.34	00.10	- 82 50 95 45	+ 82.50 107.89	02.00 117.01	- 82.50 119.01	+ 82.50 II9.42	00 10 110 01	+ 82.50 119.61	TO.811 0C.20 +	00 50 110 61	+ 82.50 120.11	+ 82.50 126.97	00.00	+ 83 00 76 98	+ 83.00 80.81		+ 83 00 80 82	- 83.00 81.33	00.00	25 CB 00 EB +	+ 83.00 82.77	03.00 02.01	00.00	+ 62 00 62 65	+ 83.00 83.09	- 83.00 83.18	+ 83.00 84.23	000000000000000000000000000000000000000	+ 83 00 85 12	+ 83.00 87.20	+ 83.00 88.60	00.00	- 93 00 96 31	53 30 00 FB +	+ 83.00 97.23	+ 83.00 105.46	00.00	+ 83 nn 107 91	+ 83.00 123.16	+ 03.00 L23.20		4 83 00 123 34	- 83.00 125.14	T 03.00 132.33	00.00 101.11	+ 83 00 134 24	+ 83.50 77.10	9 00.00 /0.40	2 50 70 /5	+ 83.50 82.24	+ 83.50 82.78	- 63.30 63.39	מיז כמ כמ כמ	- 83.50 110.28	+ 83.50 117.36	+ 83.50 119.03		+ 93 50 110 03	+ 83 50 110 03	4 83 50 110 30	+ 83.50 122.86	+ 83.50 125.65	0 + 82 EO 12E EE	
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+ 82.00 108.34 1.1e+03 9630	+ 82.00 120.51 238.26 2681	+ 82.00 120.34 223.31 230. + 82.00 120.71 232.09 2624	± 80 00 120 04 225 31 2561	+ 82 00 123 80 156 29 1898	+ 82.00 124.14 149.49 1830	+ 82.00 124.92 135.35 1687	+ 82.00 129.11 79.06 1086	+ 82.00 131.97 54.77 804	+ 82.00 132.33 52.29 774	+ 82.00 132.37 52.04 771	+ 82.00 I33.21 46.73 706	+ 82.00 134.02 42.09 048	+ 82.00 134.08 41.// 844	1 02.30 /3.02 0.16TO# 34330	. 00 50 75 00 10 00 00 00 00 00 00 00 00 00 00 00	- 82.50 76.23 6.9e+04 30799	+ 82.50 76.35 6.8e+04 30429	+ 82.50 77.09 6.2e+04 28149	- 82.50 77.57 5.8e+04 26766	- 82.50 //.8/ 5.6e+04 25946	00.00 70.40 4.00.04 640.0	- 83 50 70 40 4 60±04 21870	- 82.50 81.65 3.5e+04 17437	+ 82.5U 82.1b 3.3e+U4 1b51b	- 00 TO 00 TO 0 TO 0 TO 10 TO	+ 82.50 82.18 3.36+04 16497	+ 82.50 82.57 3.1e+04 15834	CO27T \$0+86.7 \$0.09 OC:78 -	1 00 EO OE OA O 30-EOA 1030E	- 82.50 93.34 7.8e+03 51065	00.00 90.40 0.40.00 00.74	- 80 KD QK /K K 26+D3 3K77/	+ 82.50 107.89 1.2e+03 11069	00.00 FED.01 60.07 CHAP	- 82.50 119.01 288.67 3441	+ 82.50 II9.42 2/3.99 329/		+ 82.50 119.61 267.31 3231	+ 02.50 II9.01 207.31 3231	ייייי די ד	+ 82.50 120.11 250.64 3065	+ 82.50 126.9/ 104.08 1492	00.00 70.00 10.00 1.00	+ 83 00 76 98 6 36+04 31228	+ 83.00 80.81 3.9e+04 20881		+ 83 00 80 82 3 8e+04 20864	- 83.00 81.33 3.6e+04 19//u		70871 10+ac r rr ca no ra +	+ 83.00 82.77 3.0e+04 16999	03.00 04.01 3.0ETO# 10930	1 00.00 04.00 0.00 1.00 HOTOL	+ 93 00 93 90 3 00+04 16791	+ 83.00 83.09 2.9e+04 16435	- 83.00 83.18 2.9e+04 16281	+ 83.00 84.23 2.3E+04 14302		+ 83 00 85 12 2 26+04 13278	+ 83.00 87.20 1.7e+04 10672	+ 83.00 88.60 1.4E+04 92118	00.00 00.0F 0.00.00 40.00	- 93 00 96 31 5 3e±03 40969	4 A3 00 96 63 5 1e+03 39649	+ 83.00 97.23 4.7e+03 37218	+ 83.00 105.46 1.66+03 156/0	- 00 00 101 1 1 10 00 11 11 11 10 10 10 1	+ 83 00 107 91 1 24+03 12119	+ 83.00 123.16 169.50 2440	+ 63.00 123.20 108.65 2430	. 00 00 100 00 100 00	+ 83 00 123 34 165 61 2394	- 83.00 125.14 131.59 1983	T 00.00 132.33 32.20 331	00.00 100.00 70.00	+ 83 00 134 24 40 94 762	+ 83.50 77.10 6.2e+04 33810	4 - 00.00 /0.40 0.40TO# 690#0	A 02 50 70 AS S 20+0A 202A2	+ 83.50 82.24 3.2e+04 19701	+ 83.50 82.78 3.0e+04 18633	= 03.30 03.39 4.7em04 17113	00.00 00.00 00.00	- 83.50 110.28 884.50 10358	+ 83.50 117.36 356.90 4925	+ 83.50 119.03 288.14 4133	- CU.UC HHU.CU MCC.H4 HHUC	+ 93 50 110 03 300 14 4133	+ 83 50 110 03 288 14 4133	+ 83 50 110 30 274 83 3076	+ 83.50 122.86 176.32 2764	+ 83.50 125.65 123.23 2061		
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5 Human DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                            alIleAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGTGCTCACTTAGCAGGACAGTCTATATTATCAGGATATTCCACTTACT
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                                                                                                  AGTTAAGAGGCAGATATTTTCAGACTATCAGTCAGAGGTTGACATATATA
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M35581.1 GI:150458 enterotoxin; lta gen Plasmid P307 (clone: Plasmid P307

(clone:

PAT153.) DNA.

Plasmid P307 (from

E.coli)

heat-labile gd

enterotoxin

BCT 24-APR-1996 subunit A (1ta)

777

DNA

complete

cds.

M35581 gene,

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Ratio: 5.433
Percent Similarity: 100.000
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alIleAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyr 150
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Dykes, C.W., Halliday, I.J., Hobden, A.N.,
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136 c 164 g 222 t
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SOURCE
                                 alignment_scores:
Quality:
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VERSION
                                                                                                           BASE COUNT
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LOCUS A04913
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Ratio: 5.433
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A0491
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Escherichia coli
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Patent: EP 0145486-A 5 19-JUN-1985;
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Hayes, M.V., Harford, S. and Ross, G.W.
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5.433
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Percent Identity:

100.000

Align seg 1/1 to: A04913

from:

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                                                                                                                                                                                                                                               GluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLy 217
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p370.
Plasmid ENT
plasmids.
                               M15362.1 GI:148337
LTp gene; heat-labile
Plasmid ENT (enterotox
                                                                            ENSLTPA
Plasmid ENT P307
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                             (enterotoxigenic
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E.coli)
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                                                                                       26-APR-1993
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        yrIleTyrValIleAlaThrAlaProAsnMetPheAsnValAsnAspVal

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                                                                                                                                                                                                                                                                                                                                GAACTCAAATGAATATTAATCTTTATGATCACGCGAGAGGAACACAAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATGGCGACAGATTATACCGTGCTGACTCTAGACCCCCAGATGAAATAAA
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                                                                                                                                   ATATATATGTTATAGCGACAGCACCAAATATGTTTAATGTTAATGATGTA
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Ratio: 5.433
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149 c 181 g
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150

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BASE COUNT
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LOCUS ENRLTPA
DEFINITION Plasmid ENT-
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M15361.1 GI:148333
LTp gene; heat-labile toxin.
Plasmid ENT-R (enterotoxigenic E.coli porcine isolate) DNA, clone
                                                                                                                                                                                                                                                                                                                                                                                    i (bases 1 to 898)
Yamamoto,T., Gojobori,T. and Yokota,T.
Evolutionary origin of pathogenic determinants
Escherichia coli and Vibrio cholerae Ol
J. Bacteriol. 169, 1352-1357 (1987)
Unreported.
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Plasmid ENTR
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Asmid ENT-R pCG86 (enterotoxigenic E.coli) LTp subunit A
                                                                                                                                                                                                                                                                                                                                                           copy of sequence [1] kindly provided
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ACAGAATTCGGGATGAATTA
                       snArgIleArgAspGluLeu
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seq_documentation_block:

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REFERENCE
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Percent Similarity: 100.000
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              yGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyV
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                                                                                                                          ATATATATGTTATAGCGACAGCACCAAATATGTTTAATGTTAATGATGTA
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TGGAATACCATATTCTCAGATATATGGATGGTATCGTGTTAATTTTGGTG
                                                           TTAGGCGTATACAGCCCTCACCCATATGAACAGGAGGTTTCTGCGTTAGG
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1 (bases 1 to 777)

Hayes, M.V., Harford, S. and Ross, G.W. Microbiological process
Patent: EP 0145486-A 7 19-JUN-1985;
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135 c 164 g 222 t 1 others
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HNEYFDRGTGMNILYDHARCTQTGFVRYDDGYVXTSLSLRSAHLAGQSILSGYSTYY
IYVLATAPHNENVNDVTLGVYSPHPYBDGEVSALGGIPYSGJYGMYRVNGYUDBELHN
REYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCGNSSRTITGDTCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA00403.1"
/db_xref="GI:412520"
/translation=""""
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1. .777
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/product="labile toxin
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REFERENCE
AUTHORS
TITLE
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ACCESSION
VERSION
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ORGANISM
                 FEATURES
                                                                                                                                                                                                                                                                                                                                       COMMENT
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                                                                                                         Patent: JP 198600
GLAXO GROUP LITD
OS Escherichia
PN JP 198600500
PD 10-7AN-1986
PF 12-DEC-1983
PR 12-DEC-1983
PR 12-DEC-1983
PI MAIKURU BIKK
PI GOODON UIRIK
PI GOODON UIRIK
PC C07K15/04, AK
PC C12R1:19),
PC (C12R1:9),
PC (C12R1-19),
CC strandedness
CC topology: Li
CC topology: Li
CC anti-sense:
FH Key
FT CDS
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E00613.1 GI:2168892
JP 1986005097-A/1
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Escherichia coli
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JP 1986005097-A/1
10-JAN-1986
12-DEC-1984 JP 1984262645
12-DEC-1983 GB 83 8333131
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GOODON UIRIAMU ROSU
CO7K15/04,A61K39/108,C12N1/20,C12N15/00//C12P21/00,(C12N1/20,
                                           mutation
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topology: Linear;
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replace(236,'T')
/note='SDMI'.
Location/Qualifiers
1. .777
                                                    /product~'A component toxin,LTA'
                                                                                          /product='A component toxin,LTA'
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/organism="Escherichia coli"

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BASE COUNT
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US-09-528-682-1 x E00613
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                                     AGTTAAGAGGCAGATATTTCAGACTATCAGTCAGAGGTTGACATATATA
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Ratio: 5.408
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GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr
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Tsujl.T., Inoue,T., Miyama,A., Okamoto,K., Honda,T. and i A single amino acid substitution in the A subunit of Escleoli enterotoxin results in a loss of its toxic activity J. Biol. Chem. 265 (36), 22520-22525 (1990)
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/product="heat-labile enterotoxin subunit A"
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/specific_host="Escherichia
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Patent: JP 1992079898-A 1 1
KITASATO INST:THE
OS ESCHEICHIA COLI
PN JP 1992079898-A/1
PD 13-MAR-1992
PF 23-JUL-1990 JP 1990194
PI DANBARA HIROFUMI, ABE
PC C12Q1/68,C07H21/02,C07
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JP 1992079898-A/1.
Escherichia coli.
Escherichia coli
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1 (bases 1 to 1148)
Danbara, H. and Abe, A.
DANA AND RNA PROBE TO SIMULTANEOUSLY DETECT VIBRIO CHOLERATE AND ENTEROTOXIGENIC ESCHERICHIA COLI AND DETECTION OF VIBRIO CHOLERA AND ENTEROGEXIGENIC ESCHERICHIA COLI USING THE SAME DNA AND RNA
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23-JUL-1990 JP 1990194208
DANBARA HIROFUMI, ABE AKIO
C12Q1/68,C07H21/02,C07H21/04,C12N15/11,C12N15/31,C12Q1/04,
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PC (C12N15/31,C12R1:19),(C12Q1/04,C12R1:63,C12R1:19); CC
strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: clone-pKAD008;
FH Key Location/Qualifiers
FH misc_feature 1. 1148
FT misc_feature 1. 1148
FT misc_feature 1. 1148
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TGGAATACCATATTCTCAGATATATGGATGGTATCGTGTTAATTTTGGTG
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                                                                                                                                                                                                                                                                                    Tamura,S., Asanuma,H., Tomita,T., Komase,K., Kawahara,K., Danbara,H., Hattori,N., Watanabe,K., Suzuki,Y., Nagamine, Alzawa,C., Oya,A. and Kurata,T. Escherichia coli heat-labile enterotoxin B subunits suppl with a trace amount of the holotoxin as an adjuvant for n
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-MAR-1998) Katsuhiro Komase, The Kitasato Institute, Center for Basic Research, Lab. of Virology; Shirokane 5-9-1, Center for Basic Research (Lab. of Virology; Shirokane 5-9-1, Minato-ku, Tokyo 108-6642, Japan (E-mail:komase-k@kitasato.or.jp, Tel:+81-3-3444-6637)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia.
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                                                                                                              /gene=
91. .8
                                                                                                                                             /organism="Escherichia coli"
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91..867
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                                                                            /codon_start=
                                                                                               /gene="LTh a subunit"
                                                                                                                 . 867
                                                                                                                              "LTh a subunit"
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US-09-528-682-1 x AB011677
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                                                           yGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyV
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99.583
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1DKLCYWNNKTPNSIAAISMEN"
258 c 286 g 402 t
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864. .1238
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/protein_id="BAA25726.1"
/db_xref="GI:3062902"
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IYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRN
REYRDRYYRNLNIAPAEDGYKLAGFPPDHQAWKEEPWIHHAPQGCGNSSRTITDDTCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="LTh b subunit"
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REFERENCE
AUTHORS
TITLE
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ORGANISM
                          alignment_block:
US-09-528-682-1 x ECOTOXA
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LOCUS ECOTOXA
                                                                                                        alignment_scores:
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Ratio: 5.362
milarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            This heat-labile enteroroxin is pathogenic for humans (LTh). Compared in [1] with LTp A and CT A (LTp-pathogenic for pigl CT-cholera toxin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 934)
Yamamoto,T., Tamura,T. and Yokota,T.
Primary Structure of heat-labile enterotoxin
Escherichia coli pathogenic for humans
J. Biol. Chem. 259, 5037-5044 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli
Escheria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enterotoxin; heat-labile enterotoxin; toxA gene.
E.coli H10407 (serotype 078:H11) plasmid DNA, clone pJY27.
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212. .78
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/db_xref="taxon:562"
158. .934
                                                                                                                                                                       /product="heat-labile enterotoxin A2"
                                                                                                                                                                                      /product="heat-labile
794..931
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KEYWORDS
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LOCUS S60731
                                                                                                                                           seq_name: gb_ba:S60731
                                                                 ACCESSION
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Escherichia coli 21d.
Escherichia coli
Bacteria; Proteobacteria;
                                                              subunit [Escherichia S60731
                                                                                          heat-labile enterotoxin A subunit,
                                                   S60731.1 GI:408994
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 gamma
 subdivision;
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heat-labile ent
ncmic, 1275 nt].
  Enterobacteriaceae;
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US-09-528-682-1 x S60731
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Ratio: 5.362
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                                                               GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr
ACGTTCCGGAGGTCTTATGCCCAGAGGGCATAATGAGTACTTCGATAGAG
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93252225
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Inoue,T., Tsuji,T., Koto,M., Imamura,S. and Miyama,A.
Amino acid sequence of heat-labile enterotoxin from chicken
enterotoxigenic Escherichia coli is identical to that of hun
strain, H 10407
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841. 1215
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1 227 c 248 g 364 t
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translation presented here differs from translation
publication; LTC A subunit"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="This sequence comes
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LOCALION/QUALIFIERS
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alignment_scores:
Quality: 1183.00
Ratio: 5.189
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                                                                    ATTAGCGTATACAGCCCTCACCCATATGAACAGGAGGTTTCTGCGTTAGG
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               allleAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyr 150
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                                                         TGGAATACCATATTCTCAGATATATGGATGGTATCGTGTTAATTTTGGTG
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Ratio: 5.189
milarity: 95.000
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Domenighini,M., Rappuoli,R., Pizza,M. and Hol,W.
Immunogenic detoxified mutants of cholera toxin and of tIT, their preparation and their use for the preparation Patent: US 6149919-A 5 21-NOV-2000;
Location/Qualifiers
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AR118597
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tion of vaccines
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ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh

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BASE COUNT
ORIGIN
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AUTHORS
TITLE
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US-09-528-682-1 x ECELTA
                                                                        alignment_scores:
Quality: 1183.00
Ratio: 5.189
Percent Similarity: 95.000
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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V00275.1 GI:41339
enterotoxin; signal peptide.
Escherichia coli.
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Spicer, E.K. and Noble, J.A.
Escherichia coll heat-labile enterotoxin.
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Biol. Chem. 257 (10), 5716-5721 (1982)
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84 a 142 c 179 g 263 t
ECELTA
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90. .143
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                  Vibrio cholerae.
Vibrio cholerae
                                                            Vibrio cholerae strain 1322-69
AF452584
Bacteria; Proteobacteria;
1 (bases 1 to 777)
                                                  AF452584.1
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                                                                                AAGTGCCCACTTAGTGGGTCAAACTATATTGTCTGGTCATTCTACTTATT
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Ratio: 4.836
milarity: 94.167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                                                                                                                                                                                                                                                                                         Li,M., Chen,Y., Kotetishvili,M., Stine,O.C., Morris,J.G. Jr., Sulakvelidze,A. and Sozhamannan,S. Genetic Analysis of the Virulence Regions, CTX f prophage and Vibrio Pathogenicity Island (VPI), in Diverse, Non-epidemic Serogroup Strains of Vibrio cholerae
                                                                                                                                                                                            Direct Submission
Submitted (27-DEC-2001) Department of Epidemiology and Preventive Medicine, University of Maryland School of Medicine, and VA Maryland Health Care System, The Warehouse at Camden Yards, 322 W. Camden Street, Suite 675, Baltimore, MD 21201, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae
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AF463400
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                                                                                                                                                                                                                                                                                                                                                      Unpublished
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/gene="ctxA"
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IYVIATAPNMETVINDVLGAYSPHPDEDEVSALGGIPSQIYGMYRVHFGVLDEQLHRN
RGYRDRYYSNLD1APAADGYGLAGFPPEHRAMREEPWIHAPPGCGNAPRSSMSNTCD
EKTOSLGVKFLDEYQSKVKRQIFSGYQSDIDTHNRIKDEL"
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Genetic Analysis of the Virulence Regions, CTX f prophage an Vibrio Pathogenicity Island (VPI), in Diverse, Non-epidemic Serogroup Strains of Vibrio cholerae
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Li,M., Chen,Y., Kotetishvili,M., Stine,O.C., Morris,J.G. Jr.,
Sulakvelidze,A. and Sozhamannan,S.
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/strain="203-93"
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seq_documentation_block:
LOCUS VIBCTXARA
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                                                                                                                                                                             gb_ba:VIBCTXABA
                                       DNA, clone pKY310. Vibrio cholerae
                                                              D30052.1 GI:487332
ADP-ribosyltransferase; cholera toxin.
Vibrio cholerae (sub_species O37, stra
                                                                                                                            Vibrio cholerae ctxA
  Yamamoto, K.,
                                                                                                     D30052
                          Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                 complete cds.
(bases 1 to 1372)
mamoto, K., Do, V.G.,
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 Хu,М.,
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me and ctxB
Iida,T.,
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 Miwatani,T.,
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AUTHORS
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alignment_block:
US-09-528-682-1 x VIBCTXABA
1 AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comparison of cholera toxin genes (ctxAB) of non-O1 vibrio cholerae strains 854 (O139-bengal) and S7 (O37) from two outbreaks unpublished (1994)
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Institute for Microbial Diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto, K.
Direct Submission
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06-879-8277
                                                                 VIBCTXABA
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/protein_id="BAA06289.1"
/db_xref="GI:808900"
/db_xref="GI:808900"
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VEKLCYMNKTPHAIAAISMAN"
886. .948
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94.167
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886. .1260
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RGYRDRYYSNLDIAPAADGYGLAGFPPEHRAMREEPPIHHAPPGCGNAPRSSMSNTCD
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113. .889
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/db_xref="taxon:666"
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LOCUS A16422
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          AUTHORS
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| AGTGCCCACTTAGTGGGTCAAACTATATTGTCTGGTCATTCTACTTATT
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                          Vibrio cholerae.
Vibrio cholerae
Bacteria: Proteobacteria;
1 (bases 1 to 723)
                                                                                       A16422
A16422.1 GI:641010
IMMUNOGENIC DETOXIFIED MUTANTS OF CHOLERA TOXIN AND OF 1 LT, THEIR PREPARATION AND THEIR USE FOR THE PREPARATION
                                                                                                             A subunit of cholera
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                                          gamma subdivision; Vibrionaceae;
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VACCINES
                                           Vibrio.
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eProProAspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaP
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                            AGTAACTTAGATATTGCTCCAGCAGCAGATGGTTATGGATTGGCAGGTTT
                                           ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh
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Location/Qualifiers
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/db_xref="GI:641011"
/db_xref="GI:641011"
/translation="NubtradderpedeikQSGGLMPRGQSEYFDRGTQMNINLYDH
ARGTQTGFYRHDDGYVSTSISLRSAHLVGQTILSGHSTYYIVIATAPNMFNVNDVLG
AYSPHPDEQEVSALGGITYSQIYGWYRVHFGVLDEQLHRNRGYRDRYYSNLDIAPAAD
GYGLAGFPPEHRAWREEPWIHHAPPGCGNAPRSSISNTCDEKTQSLGVKFLDEYQSKV
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125 c 163 g 20
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/db_xref="taxon:666"
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US-09-528-682-1 x AR118598
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                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
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Domenighini.M., Rappuoli,R., Pizza,M. and Hol,W.
Immunogenic detoxified mutants of cholera toxin and of the
LT, their preparation and their use for the preparation of
Patent: US 6149919-A 7 21-NOV-2000;
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AR118598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown.
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Gaps: 0
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AUTHORS
TITLE
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KEYWORDS
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LOCUS E00132
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          patent: JP 1883222033-A 1 23-DEC-1983;
SMITH KLINE RIT
OS Cholera(Vibrio)
PN JP 1983222033-A/1
PD 23-DEC-1983
PF 23-MAY-1983 JP 1983091416
PR 24-MAY-1982 US 82 381083
PI ARUFUOORU NIJIERU, DO BUIRUDO MISHTE
PC A61K39/106,A61K39/00,C07H21/04,C12N1
CC strandedness: Double;
CC topology: Linear;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FH Key Location/Qualifiers
FH CDS 1.777
FT CDS 1.777
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Arufuooru,N. and Do,B.M. .
SUBUNIT A AND B OF DNA ARRANGEMENT, RECOMBINED DNA, CHOLERA TOXIN
                                                                                                                                                                                                                                                                                                                                                                      E00132.1 GI:2168431 JP 1983222033-A/1.
                                                                                                                                                                                                                                                                                                                                                                                                               DNA coding of cholera toxin.
mat_peptide
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                                                                                                                                       23-MAY-1983 JP 1983091416
24-MAY-1982 US 82 381083
ARUFUCORU NIJIERU, DO BUIRUDO MISHIERU
A61K39/106_A61K39/00,C07H21/04,C12N15/00;
 /product='subunit A of cholera toxin'
                                                      Location/Qualifiers
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DNA

linear

PAT 29-SEP-1997

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BASE COUNT
ORIGIN
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US-09-528-682-1 x E00132
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                gSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyTyrSerThrTyrT
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AAGTGCCCACTTAGTGGGTCAAACTATATTGTCTGGTCATTCTACTTATT
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                                                                                                                                                                                        alTleAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyr 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGATGATAAGTTATATCGGGCAGATTCTAGACCTCCTGATGAAATAAA 104
                                               roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn
                                                                               LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGTCAGGTGGTCTTATGCCAAGAGGACAGAGTGAGTACTTTGACCGAG
                                    CGCCGGGTTGTGGGAATGCTCCAAGATCATCGATGAGTAATACTTGCGAT
                                                                                                                               AGTAACTTAGATATTGCTCCAGCAGCAGATGGTTATGGATTGGCAGGTTT
                                                                                                                                                                           Quality: 1088.00
Ratio: 4.814
nilarity: 94.167
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/db_xref="taxon:32644"
184 c 235 g 34
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VERSION
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                                                       mat_peptide
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mat_peptide
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Vibrio cholerae
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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Dams, E., De Wolf, M. and Dierick, W.
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  1005. .1313
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/ 205 c 276 g 426 t
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                                                                                                                                                                                                                                                                                                                                                      EKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDTHNRIKDEL"
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alignment_scores:
Quality: 1088.00
Ratio: 4.814
seq_name:
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gb_ba:VIBCTXABB
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Submitted (29-APR-1994) Koichiro Yamamoto, Osaka University,
Institute for Microbial Deseases, Department of Bacterial
Infections; 3-1 Yamadaoka, Suita, Osaka 565, Japan
(Tel:06-879-4066)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comparison of cholera toxin genes (ctxAB) of non-Ol vibrio cholerae strains 854 (Ol39-bengal) and S7 (O37) from two outbreaks Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP-ribosyltransferase; cholera toxin.
Vibrio cholerae (sub_species O139-Bengal, strain 1854) (library: plasmid) DNA, clone pKY340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Institute for Microbial Diseases Osaka University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koichiro Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-Apr-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto, K., Do, V.G., Xu, M., Iida, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'amamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 1369)
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   449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Osaka 565
   þ
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110. .886
/gene="ctxB"
214 c
                                                                                                                                                                                                                                                                                                           110.
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="plasmid"
110. .886
                                                                                                                                                                                                                                                                                                                             EKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDTHNRIKDEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .1369
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/db_xref="taxon:666"
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/strain="1854"
                                                                                                                                                                                                                                                                                       /gene="ctxA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="ctxA"
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     269
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d ctxB gene for cholera
   437
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toxins,
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alignment_block:
US-09-528-682-1 x VIBCTXABB
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seq_name:
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                                                                                                                                                               184
                                                            814
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                                                                                                                                                                                                                                     ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr 67
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                                   snArgIleArgAspGluLeu 240
                                                                     sValLysArgGinIlePheSerAspTyrGlnSerGluValAspIleTyrA
                                                                                                             GluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLy
                                                                                                                                                                                                                           AGTAACTTAGATATTGCTCCAGCAGCAGATGGTTATGGATTGGCAGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGATTTGTTAGGCACGATGATGGATATGTTTCCACCTCAATTAGTTTGAG
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                   ATAGAATTAAGGATGAATTA 883
                                                           AGTTAAAAGACAAATATTTTCAGGCTATCAATCTGATATTGATACACATA
                                                                                                                                                                                  CCCTCCGGAGCATAGAGCTTGGAGGGGAAGAGCCGTGGATTCATCATGCAC
gb_ba:VCTOXAB56
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Ratio: 4.814
milarity: 94.167
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REFERENCE
AUTHORS
TITLE
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KEYWORDS
SOURCE
                                                             alignment_scores:
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AUTHORS
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ORIGIN
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                alignment_block:
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LOCUS VCTOXAB56
US-09-528-682-1 x VCTOXAB56
                                                  Percent Similarity:
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-10_signal
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mat_peptide
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Dams, E., De Wolf, M. and Dierick, W.

Nucleotide sequence analysis of the CT operon o cholerae classical strain 569B

Biochim. Biophys. Acta 1090 (1), 139-141 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Direct Submission
Submitted (25-MAR-1991) E. Dams, Laboratory
Submitted (75-MAR-1991) Gruenenburgerlaan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V.cholerae genes for toxin proteins X58785 X55782 X58785.1 GI:48888
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                                                                                                                                                                       460
                                                1088.00
4.814
94.167
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977. .1351
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207 c 281 g 449 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDTHNRIKDEL!
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                                                                                                                                                                                                       1040. .1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
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Align seg 1/1

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VCTOXAB56

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REFERENCE
AUTHORS
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ORGANISM
                                                                                                     DEFINITION ACCESSION
                                                                                                                                  seq_documentation_block:
LOCUS VCCTX
                                                                                                                                                                            seq_name: gb_ba:VCCTX
                                                                          KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy
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                                           Vibrio cholerae.
Vibrio cholerae
                                                                                                     Vibrio cholera toxin (ctx) operon x00171
1 (bases 1 to 2020)
Mekalanos, J.J., Swar
                                                                        overlapping genes; signal peptide;
                                                                                         X00171.1 GI:48347
                              Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio
 Swartz,D.J.,
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 Pearson, G.D., Harford, N.,
                                                                                                                    DNA sequence
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 Groyne, F.
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BASE COUNT
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Ratio: 4.814
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Cholera toxin genes: nucleotide sequence, deletion analysis and vaccine development
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1352. .1660
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/note="-10 region"
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RGYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIHHAPPGCGNAPRSSISNTCD
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| AGTGCCCACTTAGTGGGTCAAACTATATTGTCTGGTCATTCTACTTATT
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JP 1992099488-A/17.
synthetic construct
synthetic construct
artificial sequence.
 PRIMER FOR AMPLIFICATION OF GENE Patent: JP 1992099488-A 17 31-MAR-1992;
                        Shirai, H.
                                                                                                           Cholera toxin gene. E03512
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PN JP 192099488-A/17
PD 31-AMAR-1992
PF 20-AMG-1990 JP 1990219523
PF 20-AMG-1990 JP 1990219523
PI SHIRAI HIROMASA
PC C12N15/11.C12Q1/68;
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qu
FH Key Location/Qu
FH misc_feature 1. 2020
FT misc_feature 1. 2020
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3480 bp DNA linear BCT 15-NO Vibrio cholerae accessory cholera enterotoxin (ace), zonular occludens toxin (zot), cholera enterotoxin A-subunit (ctxA), cholera enterotoxin B-subunit (ctxB) genes, complete cds. AF175708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloning and nucleotide sequence analysis of the virulence cassette from Vibrio cholerae KNIH002 isolated in Korea Misainmurhag Hoiji 35 (3), 205-210 (1999)
2 (bases 1 to 3480)
Shin, H.J., Park, Y.C. and Kim, Y.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-AUG-1999)
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Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         South Korea
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287. .5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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                                                                                                                                                                                                  enterotoxin"
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Align seg 1/1 to: AF175708
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                                                                                                                                                                                                          2126 AAGTGCCCACTTAGTGGGTCAAACTATATTGTCTGGTCAITCTACTTATT
                                                                                                                                                                                                                                                                                                                                                                             2026 GAACTCAAATGAATATCAACCTTTATGATCATGCAAGAGGAACTCAGACG
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                                                                                                                                             yrīleTyrValIleAlaThrAlaProAsnMetPheAsnValAsnAspVal 100
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                                         TTAGGGGCATACAGTCCTCATCCAGATGAACAAGAAGTTTCTGCTTTAGG
                                                                                                                           ATATATATGTTATAGCCACTGCCCCCAACATGTTTAACGTTAATGATGTA
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1872. 2648
/gene="ctxA"
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VEKLCYWNNKTPHAIAAISMAN"
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2645. .3019
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RGYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIHHAPPGCGNAPRSSMSNTCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="cholera enterotoxin B-subunit"
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FFETESGSVPTELFASSYRYKVLPLPDFNHFVVFDTFAAQALWVEVKRGLPIKTENDK
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The entire core region of the ctx-phi (ctx-prophage)
environmental strain of V. cholerae
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Viruses; ssDNA viruses; Inoviridae; Inovirus
1 (bases 1 to 4275)
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                                                                                                                                                                                                                                                                                                                             Submitted (27-AUG-2001) Microbiology,
                                                                                                                                                                                                                                                                                                                                                Bhattacharyyaa, T., Nandy, R.K. and Nair, G.B. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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CtxB (ctxB)
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yrIleTyrValIleAlaThrAlaProAsnMetPheAsnValAsnAspVal 100
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4.814
94.167
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AUTHORS AUTHORS Heidelberg,J.F., Eisen,J.A., Nelson,W.C., Clayton,R.A., Gwinn,M.L., Dodson,R.J., Haft,D.H., Hickey,E.K., Peterson,J.D., Umayam,L.A., Gill,S.R., Nelson,K.E., Read,T.D., Tettelin,H., Richardson,D., Ermolaeva,M.D., Vamathevan,J., Bass,S., Qin,H., Dragoi,I., Sellers,P., McDonald,L., Utterback,T., Fleishmann,R.D., Nierman,W.C., White,O., Salzberg,S.L., Smith,H.O., Colwell,R.R., Mekalanos,J.J., Venter,J.C. and Fraser,C.M. TITLE Direct Submission Submitted (14-JUN-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA	Vib. Vib. Bac 1 Hei Hei Dodd Gill Erm Sel. Nie Nie DNA Chol Natu	seq_name: gb_ba:AE004224 seq_documentation_block: LOCUS AE004224 10646 bp DNA linear BCT 31-JUL-2000 DEFINITION Vibrio cholerae chromosome I, section 132 of 251 of the complete chromosome. ACCESSION AE004224 AE003852 VERSION AE004224.1 GI:9655952 KEYWORDS	217 sVallysargGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA 234	16/ PEPOPEOSSPHISCHALGEIPAEGGLUGLUFOTEPILEHISHISALAP 184	ATATATATGTTATAGCCACTGCACCCAACATGTTAAACGTTAATGATGTA LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl
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CDS

gene

SdS

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                                                                                                                                                                                                                                                                                                                                                                                        complement(5762. .7045)
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KGLNSIF"
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4073 GCAGTCAGGTGGTCTTATGCCAAGAGGACAGAGTGAGTACTTTGACCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy
GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr 67
                                                                                                                                    LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl 117
                                                                                                                                                                                                                                                                                                                                                GGATTTGTTAGGCACGATGATGGATATGTTTCCACCTCAATTAGTTTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTACTCAAATGAATATCAACCTTTATGATCATGCAAGAGGAACTCAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThrGlnThr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sArgSerGlyGlyLeuMetProArgGlyH1sAsnGluTyrPheAspArgG
|::::|||||||||||||||||||||||
                                                                                   alIleAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyr 150
                                                                                                                                                                                                                                                                              ATATATATGTTATAGCCACTGCACCCAACATGTTTAACGTTAATGATGTA 3824
                                                                                                                                                                                                                                                                                                 yrIleTyrValIleAlaThrAlaProAsnMetPheAsnValAsnAspVal 100
                                                                   TTAGGGGCATACAGTCCTCATCCAGATGAACAAGAAGTTTCTGCTTTAGG
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4.814
94.167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GP:2564358;
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MFSSLKNKLNTFKSTLSLGVFLLFSAFANQALAAADAGLVTEVTKTLGTSKDTVIALGPLIMGVVGAIVLIVTVIGLIRKAK"
complement(7440. .7823)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(7440. .7823)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
/product="colorization factor"
/protein [d="AAF94618.1"
/db_xref="GI:9655962"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="VC1462"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to ; identified by sequence similarity;
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alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
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ORGANISM
                               alignment_block:
US-09-528-682-1 x VIBCTXA
                                                                                                                                                                               BASE COUNT
ORIGIN
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LOCUS VIBCTXA
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAGAATTAAGGATGAATTA 3404
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Vibrio cholerae enterotoxin Al I
K02679
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                                                                                                                                                                                 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is reported [1] to be identical El Tor 2125 and 569B. the 'ttttgat' sequence beginning at position 38 and once more at 101 the amount of enterotoxin produced in various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lockman, H.A., Galen, J.E. and Kaper, J.B.
Vibrio cholerae enterotoxin genes: Nucleotide
DNA encoding ADP-ribosyltransferase
J. Bacteriol. 159, 1086-1089 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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bp
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   ţo:
                                                                                                                                                                             upstream
   VIBCTXA
                                                                                                                                                                                                                          /translation="MVKIFVFFIFLSSFSYANDDKLYRADSRPPDEIKQSGGLMPRG QSEYFDRGTQMNINLYDHARGTQTGFVRHDDGYVSTSISLRSAHLVGQTILSGHSTYY IYVIATAPNMENVNDVLGAYSHHPDEQEVSALGGIPYSQIYGWYRVHFGVLDEQLHRN RGYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIHHAPFGCGNAPRSS" 196. .777
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Vibrio cholerae"
/db_xref="taxon:666"
142. .195
                                                                              934.00
5.049
95.855
                                                                                                                                                                                            /product="enterotoxin subunit A1" 119 c 164 g 257 t
                                                                                                                                                                                                                                                                                                       /trans1_table=11
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/db_xref="GI:155160"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                       /note="enterotoxin prepeptide"
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142. .>777
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(ctxA) gene
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REFERENCE
AUTHORS
TITLE
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ORGANISM
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LOCUS ECOETOXHL
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                                              FEATURES
                                                          COMMENT
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                                                                                                                                                                                                                                             ECOETOXHL
EScherichia coli (strain 41) heat-labile en (LT-IIb) A and B chain genes, complete cds.
                                                                                    l (bases 1 to 1262)
Pickett,C.L., Twiddy,E.M., Coker,C. and Holmes,R.K.
Cloning, nucleotide sequence, and hybridization studies
IIb heat-labile enterotoxin gene of Escherichia coli
J. Bacteriol. 171 (9), 4945-4952 (1989)
                                                                                                                                                                                          M28523.1 GI:576584
LT-IIb gene; enterotoxin
Escherichia coli (strain
Escherichia coli
                                                            ဝှ
                                                                           89359131
                                                                                                                                                                 Escherichia
                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae,
                                         Nov 28, 1994 this sequence version replaced gi:341953
Location/Qualifiers
                             1. .1262
/strain="41"
               /organism="Escherichia coll"
                                                                                                                                                                                                                                                                                  1262 bp DNA linear F (strain 41) heat-labile enterotoxin
                                                                                                                                                                                                         type IIb.
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BASE COUNT
ORIGIN
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Percent Similarity:
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                                                 TyrArgAlaAspSerArgProProAspGluIleLysArgSerGlyGlyLe
AATGATGGATATGTATCAACAACAACGACTTTGAGACAGGCTCACTTATT 38:
              AspAspGlyTyrValSerThrSerLeuSerLeuArgSerAlaHisLeuAl 72
                                                                                                                                                             TTCAGGGCTGATTCGAGAACGCCTGATGAAGTCAGACGCTCAGGGGGGGTT
                                                                                                                                                                                                                                                                                                              Quality:
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                                                                                                                                                                                                                                                                                                                                                                               /gene="LT-IIb"
/note="B chain of heat-labile enterotoxin type IIb"
/product="enterotoxin"
195 c 285 q 413 t
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894. .962
                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="msfkkiikafvimaalvsvqahagasqffkdncnrttaslvegv
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MCASPASSENVIWAIELEAE"
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894. .1262
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173. .9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MAKVISEFISLFLISFPLYANDYFRADSRTPDEVRRSGGLIPRG
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RDYRRDLFRGLSAAPNEDGYRIAGFPDGFPAWEEVPWREFAPNSCLPNNKASSDTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="LT-IIb"
113. .904
                                                                                                                                                                                                                                                                                   682.00
3.875
81.481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLTNKLSQHDLADFKKYIKRKFTLMTLLSINNDGFFSNNGGKDEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="enterotoxin"
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26. .31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="enterotoxin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="LT-IIb"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'codon_start=1
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AUTHORS
                                                                                                                                                                                                                                                                                                                                    KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_ba:ECOLTIIA
                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                              MEDLINE
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           CDS
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382 AGGGCAAAATATGCTTGGTGGGTATAATGAGTACTATATTTATGTTGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTCCTAATGAGGATGGCTATCGAATTGCTGGATTTCCCGACGGATTTCC 681
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| CAAATAATTGGCTGGTATAGAGTATCTTTCGGTGCTATAGAGGGGGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTATCACAGCATGATTTAGCTGATTTTAAGAAATATATAAAGAGAAAA 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuSerThrIleTyrLeuArgGluTyrGlnSerLysValLysArgGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               snSerSerArgThrIleThrGlyAspThrCysAsnGluGluThrGlnAsn 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCGTGGGAAGAAGTTCCCTGGAGAGAATTTGCGCCTAACTCTTGTCTAC 731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pickett,C.L., Weinstein,D.L. and Holmes,R.K.
Genetics of type IIa heat-labile enterotoxin of Escherichia co-
operon fusions, nucleotide sequence, and hybridization studies
J. Bacteriol. 169, 5180-5187 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E.coli (strain SA53) DNA.
Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                            /transl_table=11
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/protein_id="AAA24093.1"
/protein_id="AAA24093.1"
/db_xref=="Ci:146672"
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VVAPAPNLEDVNGVLGRYSPYSPSNFPAWREMPWSTFAPEQCVPNNKEFKGGVCISA
                                                   TNVLSKYDLMNFKKLLKRRLALTFFMSEDDFIGVHGERDEL*
                                                                                                                                                                                                                                                                                                                                                /organism="Escherichia
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/note="heat labile enterotoxin type IIa
                                                                                                                                                                                                                                                                        /codon_start=
                                                                                                                                                                                                                                                                                                     /note="heat labile enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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(LT-IIa) A
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                                                                                          nAlaTrpArgGluGluProTrpIleHisHisAlaProGlnGlyCysGlyA 189
                                                                                                                                                                                                                                           AlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProProAspHisGl
                                                                                                                                                                                                                                                                                           TGCAGCGAAACAGGGATTATCGAGGAGTTTATTTCGAGGGTTAACGGTT
                                                                                                                                                                                                                                                                                                                    euHisArgAsnArgGluTyrArgAspArgTyrTyrArgAsnLeuAsnIle 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProHisProTyrGluGlnGluValSerAlaLeuGlyGlyIleProTyrSe 122
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                              LeuSerThrIleTyrLeuArgGluTyrGlnSerLysValLysArgGlnIl 222
                                                                      CGAATAATAAAGAATTTAAAGGAGGGGTGTGCATTTCAGCGACAAATGTG
                                                                                                                                                                                                                      GCACCTAATGAAGATGGCTATCAACTTGCAGGGTTTCCGAGTAACTTCCC
                                                                                                                                                                                                                                                                                                                                                                    CCATATCCCAGTGAAAATGAATTTGCTGCATTAGGAGGGATTCCCTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCAGCACCAAATTTATTTGATGTGAATGGTGTTTAGGACGGTATAGT
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CTATCGAAATATGATTTGATGAATTTTAAAAAACTCTTAAAACGCAGGCT
                                                                                                                                               AGCCTGGAGAGAAATGCCATGGAGTACATTTGCTCCTGAACAGTGTGTGC
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                                mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto,T., Tamura,T., Ryoji,M., Kaji,A., Yokota,T. and Sequence analysis of the heat-labile enterotoxin subunit originating in human enterotoxigenic Escherichia coli J. Bacteriol. 152 (1), 506-509 (1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E.coli heat labile enterotoxin a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       see also other loci beginning 
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 190 to 774)
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                                              ILSYTESMAGKREMVIITFKSGATFQVEVPGSQHIDSQKKAIERMKDTLRITYLTETK
IDKLCVWNNKTPNSIAAISMEN"
                                                                                             /product="enterotoxin B"
/protein_id="AAB02982.1"
/db_xref="GI:1395122"
                                                                                                                                                                                                                                    /gene="toxB"
205. .267
                                                                                                                                                                                                                                                                     /gene="toxB"
195. .579
                                                                                                                                                                                                                                                                                                                    KVKRQIFSDYQSEVDIYNRIRNEL'
                                                                                                                                                                                                                                                                                                                                                   /product="enterotoxin A"
/protein_id="AAB02981.1"
/db_xref="GI:1395121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /specific_host="Homo
/db_xref="taxon:562"
                                                                                                                                                                                                     /gene="toxB"
205. .579
                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=2
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="H10407"
/product="enterotoxin
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                                                                                   translation="MNKVKCYVLFTALLSSLCAYGAPQSITELCSEYRNTQIYTINDK/
                                                                                                                                                 transl_table=11
                                                                                                                                                                                /gene="toxB"
                                                                                                                                                                                                                                                                                                                                     translation="AWREEPWIHHAPQGCGDSSRTITGDTCNEETQNLSTIYLRKYQS/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Escherichia coli"
                                                                                                                                                                  codon_start=1
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b (toxB)
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US-09-528-682-1 x ECOELT
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Ratio: 5.250
Percent Similarity: 100.000
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Germani,Y. and Desperrier,J.M.

Nucleotide sequence variations in genes encoding heat labile enterotoxins of Escherichia coli isolated in South Pacific Unpublished
                                                                                                                                                                                                  Direct Submission
Submitted (17-JAN-1995) Y. Germani, Institut Pasteur,
Roux, F- 75724 Paris Cedex 15, FRANCE
Related sequence: M15361-3 (Yakamoto).
                                                                                                                                                                                                                                                                                                                                                                     heat-labile enterotoxin; LT 87
Escherichia coli.
Escherichia coli
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/transī_table=11
/product="heat-labile enterotoxin"
/protein_id="CAA58800.1"
/db_xref="GI:1648866"
/db_xref="SWISS-PROT:P13811"
/translation="MNKVKFYVLFTALLSSLCAHGAPQSITELCSEYHNTQIYTINDK
                                                                                                       /gene="
205..5
                                                                                                                                /db_xref="taxon:562"
205. .579
                                                                                                                                                      /organism="Escherichia coli"
/strain="ETEC LT 87"
                                                                           codon_start=1
                                                                                           'gene="LT 87"
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Gaps: 0
Percent Identity: 95.588
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alignment_block:
US-09-528-682-1 x ECOELTA2
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                                                                                                                                                                                                                                                                                                       Spicer, E.K., Kavanaugh, W.M., Dallas, W.S., Falkow, S., Konigsberg, W.H. and Schafer, D.E. Seguence homologies between a subunits of Escherichia Vibrio cholerae enterotoxins Proc. Natl. Acad. Sci. U.S.A. 78, 50-54 (1981) 81223767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECOELTA2 165 by E.coli heat labile enterotoxin
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IDKLCVWNNKTPNSIAAISMEN"
a 105 c 113 g 151 t
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/db_xref="taxon:562"
30 c 35 g 41 t
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Percent Identity: 90.566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGATTCATCATGCACCACAAGGTTGTGGAGATTCATCAAGAACATTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rgGluTyrGlnSerLysValLys.ArgGlnIlePheSerAspTyrGlnSe 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rGluVal 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGAATATCAATCAAAAGTTATAGAGGCACATATTTTCAGACTATCAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGTGATACTTGTAATGAGGAGACCCAGAATCTGAGCACAATATATCTCA
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Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cholera toxin; CTA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Structure and arrangement of the cholera toxin cholerae 0139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (24-NOV-1993) M. Lebens, Dept. o Immunol., Goetegorgs univ., Guldhedsgatan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X76391.1 GI:433859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lebens, M. and Holmgren, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ebens, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microbiol. Lett. 117 (2),
                                                                                                                                                                                                                                                                                                                                   /gene="ctxA2"
37. 177
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                                                                                                                                                                 /product="cholera
                                                                                                                                                                                /gene="ctxB"
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37. .177
                                                                                                                                                                                                                                                                                                                                                                                                   /strain="4260B"
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                                                                                                                                                                                                                                     'db_xref="SPTREMBL:Q57372"
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                                                                                                                                                                                                                       translation="MSNTCDEKTQSLGVKFLDEYQSKVKRQYFSGYQSDIDTHNRIKD
                                                                                                                                                                                                                                                                                                                                                                                       'isolate="serotype 0139"
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                                                                                                                                        "ctxB"
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dsgatan, Ioa, 413 46 Goetebo
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prim_transcript
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V.cholerae (0139) ctxA and ctxB
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Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
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3.872
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                                                                                                                                      /gene="ctxA"
37. .177
                                                                                                                                                                                                                                     Location/Qualifiers
1. .938
                                                                                                                                                                                                        /strain="4260B"
                                                                                                                         'gene≖"ctxA"
                                                                                                          codon_start=1
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186 GlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsnGluGl
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                                                                                                                                                                                                                                                                                                                                                  Structure and arrangement of the cholera toxin cholerae {\tt O139}
                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (24-NOV-1993) M. Lebens, Dept. o
Immunol., Goetegorgs univ., Guldhedagatan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEKLCVWNNKTPHAIAAISMAN"
1 139 c 150 g 2
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37. .177
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                                                                                                                                                                                                                                                        /organism="Vibrio cholerae"
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Ioa, 413
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US-09-528-682-1 x VCCTXAB
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LOCUS A02701
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                                                                                                                                                                                          synthetic construct.
synthetic construct
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                                                                                                                     Patent:
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                                                                                                                NEW PLASMIDS AND BACTERIAL STRAINS AND PRODUCTION PROCESS THEREO PATENT: WO 8302456-A 1 21-JUL-1983;
                                                                                                                                                               artificial sequence.
1 (bases 1 to 795)
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237. .545
                                        /organism="synthetic construct"
/db_xref="taxon:32630"
1. .795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene-"ctxB"
174. .548
            /note="enterotoxoid and antigens production" 180 c 193 g 174 t 41 others
                                                                                                  Location/Qualifiers
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seq_documentation_block: LOCUS A06082

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                                                                              221 lnIlePheSerAspTyrGlnSerGluVal 230
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                            32
                            AGATATTTTCAGACTATCAGCTCAAGGTN
gb_pat: A06082
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artificial sequence.
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A02702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A02702 795 bp DNA linear Synthetic DNA sequence for enterotoxoid production
                                                                                                                                                                                                                                                                                                                                                                                                                       NEW PLASMIDS AND BACTERIAL STRAINS AND PRODUCTION PROCESS THEREO F
Patent: WO 830/456-A 2 21-JUL-1983;
Patent: WO 830/456-A 2 21-JUL-1983;
1. .795
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                                                                                                                                                                                                                                                                                                                                                     174
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                                                                                                                                                                                                                                                                                                                                                     /note="enterotoxoid and antigen production"
193 c 180 g 207 t 41 others
                                                                                                                                                                                                                                                                                                                                                                              /organism="synthetic construct"
/db_xref="taxon:32630"
1. .795
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86.047
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BASE COUNT
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US-09-528-682-1 x A06082
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                                                                                                                                                                                                         TITLE
JOURNAL
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TITLE
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                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 lnIlePheSerAspTyrGln 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    714 GAATCTGAGCACAATATATCTCAGGGAATATCAATCAAAAGTTAAGAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                gb_pat:A06083
                                                                                                                                                                                  artificial sequence.

1 (bases 1 to 791)
Ceska, M., Kricek, F., Hoegenauer, G. and Besemer, J.
Plasmids and bacteria strains, and method of preparing
Patent: EP 0084522-A 2 27-JUL-1983;
SANDOZ AG; SANDOZ-PATENT GMBH; SANDOZ-ERFINDUNGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ceska,M., Kricek,F., Hoegenauer,G. and Besemer,J. Plasmids and bacteria strains, and method of preparing Patent: EP 008452-A 1 27-JUL-1983; SANDOZ AG; SANDOZ-PATENT-GMBH; SANDOZ-ERFINDUNGEN Verwaltungsgesellschaft m.b.H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pebK620 HindII-fragment.
A06082
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A06083
                             Quality:
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l (bases 1 to 791)
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/db_xref="taxon:32630"
179 c 193 g 174 t
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/db_xref="taxon:32630"
193 c 179 g 206 t
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US-09-528-682-1 x A06083/rev
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LOCUS VIBTOX
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MEDLINE
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                                                            mat_peptide
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                                                                                                        sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The termination codon of subunit A2 overlaps the initiation codon of subunit B by 4 bp. The correct translation of the 2 subunits is the result of a shift in reading frames at this junction. Previous protein structural analysis has shown that the A2 subunit is bound to a precursor of the A subunit. Therefore, the 'met' at position is not an initiator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio cholerae toxA and toxB genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholerae (El Tor biotype strain 62746) DNA, clone pCVD002. Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cholerae enterotoxin
J. Biol. Chem. 258, 13722-13726 (1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio. 1 (bases 1 to 512)
Lockman, H. and Kaper, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enterotoxin
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    188
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199
/product="enterotoxin
9 a 74 c 88 g
upstream of NdeI site.
                                                                                                                         /translation="MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIYTLNDK
IFSYTESLAGKREMAIITFKNGAIFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTEAK
VEKLCVWNNKTPHAIAAISMAN"
                                                                                                            141. .200
                                                                                                                                                                                 /transl_table=11
/protein_id="AAA27573.1"
/db_xref="GI:155298"
                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
/protein_id="AAA27572.1"
/db_xref="GI:155297"
                                                                                                                                                                                                                                                                                                138. .512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Vibrio cholerae"
/db_xref="taxon:666"
                                                                                    /note="enterotoxin subunit B signal peptide"
                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                          /note="enterotoxin subunit
                                                                                                                                                                                                                                                                                                                                         translation="MSNTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDTHNRIKD/
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="enterotoxin subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                       subunit B
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for cholera
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                                             mature peptide"
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alignment_scores:

Quality: Ratio:

157.00 3.925

Length: Gaps:

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US-09-528-682-1 x VIBTOX
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LOCUS VIBCTA2
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Percent Similarity:
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MEDLINE
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                                                                                                                                      197
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                                                                                                                                                                                         AATACTTGCGATGAAAAACCCCAAAGTCATGGTGTAAAATTCCTTGACGA
                                                                                                                                                                                                       AspThrCysAsnGluGluThrGlnAsnLeuSerThrIleTyrLeuArgGl
                                                                                        TTGATACACATAATAGAATTAAGGATGAATTA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGATACACATAATAGAATTAAGGATGAATTA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATACCAATCTAAAGTTAAAAGACAAATATTTTCAGGCTATCAATCTGATA 106
                                                              gb_ba:ECOPHLEG5
900 bp DNA line
Escherichia coli heat-labile enterotoxin gene,
M61015
                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio. 1 (bases 1 to 251)
Gennaro, M.L. and Greenaway, P.J.
Nucleotide sequences within the cholera toxin operon
Nucleic Acids Res. 11, 3855-3861 (1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio cholerae cholera toxin subunit B 5' end.
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Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cholera toxin.
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                                                                                                                                                                                                                                                                                                           150.00
3.846
88.636
                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Vibrio cholerae"
/db_xref="taxon:666"
38 c 38 g 79 t
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Gaps: 0
Percent Identity: 63.636
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             linear
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alignment_block:
US-09-528-682-1 x ECOPHLEG5
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LOCUS A69697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 117.00
Ratio: 5.318
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                 ACGTTCCGGAGGTCTT
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Sequence 15 from Patent WO9807864
A69697
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                                                                                                                                                   FOSTER KEITH ALAN (GB)
                                                                                                                                                                                                                                                 unidentified
                                                                                                                                                                                                                                                              unidentified
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                                                                                                                                                                                                                                unclassified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/trans1_table=11
/product="heat-labile e
/protein_id="AAA24335.1
/db_xref="GI:147191"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Escherichia
/strain="K-12"
/db_xref="taxon:562"
                                                                                       /organism="unidentified"
/db_xref="taxon:32644"
                                                            /product="unnamed"
                                                                                                                                       Location/Qualifiers
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213 c 181 g 279 t
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/protein_id="CAB42522.1"
              codon_start=1
                            note="unnamed protein product"
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LOCUS BD009884
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                                                                                                                                                                                                              THORS Shone,C.C., Quinn,C.P. and Foster,K.A.

TE Recombinant toxin fragments

RNAL Patent: JP 2001502890-A 8 06-MAR-2001;

MICROSIOLOGICAL RESEARCH AUTHORITY CAMR,THE SPEYWOOD LABORATORY LTD

OS Unidentified
PN JP 2001502890-A/8
PD 06-MAR-2001
PF 22-AUG-1997 JP 1998****

PR 23-ANTO-100
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                         source
                                                             PD 06-MAR-2001
PF 22-AUG-1997 JP 1998510524
PR 23-AUG-1996 GB 9617671.4,13-DEC-1996 GB 9625996.5 PI
CLIFFORD CHARLES SHONE, CONRAD PADRAIG QUINN, KEITH ALAN FOSTER PC
C12N15/31,C12N1/21,C12P21/02,C07K14/33,A61K38/16,A61K39/08 CC
Strandedness: Double;
CC Topology: Linear;
FH Key
FT CDS
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BD009884.1 GI:18638257
JP 2001502890-A/8.
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iperdyfundeegdlwppdeakopuygydstylstynkednylkguykkferikstd
ligrultstyngiffungtekyuitunultoninviopdegsyrbeelniviigpsadi
iqfecksfehevlultrngygstqyirfspdftgegsebluviigpsadi
iqfecksfehevlultrngygstqyirfspdftgeeslevdynpllgagkfatpa
vtlahelihaghrlyciainpwrfkuntnayyemsglevsfeelrtfegehdakfids
loenefrlyyynkfkdiastlnkaksivgtraytknykkekstllsedtsgkesvd
klkfoklykmlteiytednfykffkuntnayyemsglevsfeelrtfegenskie
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grudalnngonteinmmntyklknetgeffeelystlotnieaaebnisloliog
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grudalnusyneallngsruytffssdynkkyittnwktghythethef
ehgksrialtnsyneallngsruytffssdynkkytloytmyhthlafet
ystytmybleitspspligenskmbyykyttmwkakvnooldlirkkmk
ealengaenfykalinygyneesknolngsklosklesknetydf
grylhnsmlpygykkledfdaslkoalkytytonkgtligoudrkkbynntlstdi
secolgyvynandeitgeboaskbalkytytongtligoudrkbynntlstdi
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418 c 509 g 823 t
/organism="unidentified"
                                           Location/Qualifiers
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Percent Identity: 54.762
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seq_name: gb_pat:I03425
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                                 GCAGTCAGGTGGTCTTATG
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Gennaro, M.L. and Greenaway, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio cholerae (strain El Tor 1621) DNA Vibrio cholerae
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Location/Qualifiers
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78.571
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/db_xref="taxon:666"
23 c 38 g 109 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 oProAspHisGlnAlaTrp 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AACTTAGATATTGCTCCAGCAGCAGCAGTTATGGATTGGCAGGTTTCCC 53
1 (bases 1 to 167751)

18 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Banbarda,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burnell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., David,R., David,R., David,R.L., David,R.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwalte,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Ganner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hannilton,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hennandez,J., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson, R. Tia, V. Tohneon, B. Tilvet, S. Tuda, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCGGAGCATAGAGCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_htg:AC107423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 bp ss-DNA
Sequence 1 from Patent US 4882278.
I03425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-toxinogenic vibrio cholerae mutants
Patent: US 4882278-A 1 21-NOV-1989;
President and Fellows of Harvard College;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 72) Mekalanos, J.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC107423 167751 bp
Homo sapiens chromosome 3q clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC107423.4 GI:18653537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE, 8 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cambridge, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I03425.1 GI:270622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106.00
5.048
91.304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
14 c 21 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 23
Gaps: 0
Percent Identity: 78.261
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA linear HTG 13-FEB-2002 RP11-372M20, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.C., Lewis, L.C., Lewis, L.C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucler, A., Lucler, R., Luna, R., Ma, J., Waheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Miner, G., Miner, E., McLeod, M.P., Meador, M., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, L. Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, N., Thomas, N., Thomas, N., Thomas, S., Ward, Moore, S., Warren, R., Washington, C., Walliams, G., Williamson, A., Walcz, K., Rolfed, B., Walliams, G., Williamson, A., Walcz, K., Rolfed, S., Worley, K., Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted (20-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Feb 13, 2002 this sequence version replaced gi:18581385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 8 contigs. The true order of the pleces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: Plasmid; M77789
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 163427 bases at least Q40
Consensus quality: 165469 bases at least Q30
Consensus quality: 166917 bases at least Q20
Consensus quality: 166917 bases at least Q20
Estimated insert size: 167289; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sgarose-fp estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 167751)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
         147154
154263
154363
161158
                                                                                                                                     42447
42547
71416
71516
99156
99256
124810
124910
147054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project Information
Center project name: HDRX
Center clone name: RP11-372M20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College of Medicine
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                                    124809:
124909:
147053:
147153:
154262:
154362:
161157:
                                                                                                                                                                                                                                                                                                                            42446:
42546:
71415:
71515:
s: gap of unknown length s: contig of 2554 bp in 1 gap of unknown length s: contig of 22144 bp in 1 gap of unknown length contig of 7109 bp in 1e gap of unknown length contig of 6795 bp in 1e gap of unknown length se gap of unknown length
                                                                                                                                                                                                                                                                                          contig of 42446 bp in length
gap of unknown length
contig of 28869 bp in length
gap of unknown length
contig of 27640 bp in length
      bp in length
length
                                                                                                   length
                                                                                                                                                                   length
                                                                                                                                                                                                                                  length
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JOURNAL REFERENCE AUTHORS

TITLE

TITLE JOURNAL

COMMENT

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alignment_scores:
Quality: 101.00
Ratio: 1.262
Percent Similarity: 53.691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AC107423 from: 1 to: 167751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-528-682-1 x AC107423
                                                                                                                                                                                                                                100 ValLeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLe 116
|||||||||::: ::: ||| |||:::||:::
45208 GTGCTGGGTACACTGGATATCCATATGCAGAGAATGAAACT....... 45249
                                                                      45263 CTACATACAAAAAGCAAAATCAAAATGTATTAAAATACTTAAAATTTAAGAGT 45312
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45518 ACTACTCATCTCACAAGGAATTAATAATAAGACTATATAAGGAGCTC 45564
                                                                                                                                                                                                                                                                                                                 45355 ......CCAGGACAT.....TGGAGGGGCAAAAATTTCTTG 45385
                                                                                                                                                                                                                                                                                                                                                    164 uAlaGlyPheProProAspHisGlnAlaTrpArgGluGluProTrpIleH 181
                                                                                                                                                                                                                                                                                                                                                                                                                        148 ArgTyrTyrArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLe 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 lyValIleAspGlu.....ArgLeuHisArgAsnArgGluTyrArgAsp 147
                      225 spTyrGlnSerGluValAspIleTyrAsnArgIleArgAspGluLeu 240 ::|||:::|||::: | | | | | | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 uGlyGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
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Location/Qualifiers
1. .167751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism "Homo sapiens"
/db_xref "taxon:9606"
/chromosome="39"
/chone="rpp11-372M20"
30864 c 31135 g 50585 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 24.832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         701 others
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| SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051317 + 117 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051317 + 117 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051317 + 117 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051326 + 117 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051326 + 117 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051316 + 117 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051316 + 117 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051316 + 117 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051318 + 117 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051314 + 117 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051314 + 117 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051324 + 117 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051324 + 117 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051322 + 117 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051323 + 117 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051157 + 107 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051159 + 107 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051159 + 107 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051159 + 107 | SIDSS/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAA051133 + 107 | SIDSS/gcgdata/geneseq/geneseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS5/gcgdat
/SIDS5/gcgdat
/SIDS5/gcgdat
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/SIDS5/gcgdat
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Query: US-09-528-682-1
Query length: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM of: US-09-528-682-1 to: N_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            score_list:
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search time (sec):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -MODEL-frame+_p2n.model -DEV-x1p
-q-/cgn2_1/USPTO_spool/US99528682/runat_18062002_082444_7843/app_query.fasta_1.689
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-GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIDS5/gcgdata/geneseq/geneseqn-embl/NA19
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-TRANS-human40.cdi -LIST-1000 -DOCALIGN-200 -THR_SCORE-pct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jun 18, 2002 7:38 PM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ta/geneseq/geneseqn-embl/NA1993.DAT:AAQ42768 + 1183.00 2269.;
ta/geneseq/geneseqn-embl/NA1999.DAT:AAV81595 + 1183.00 2269.;
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6 + 1287.00 2469.79

7 + 1283.00 2462.06

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4 + 1280.00 2456.26

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/genesegn-embl/NA2001A.DAT:AAI99682
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                                                                                     BIOTECHNOLOGY RES INST.
                                                                                                                                          99WO-KR00555
                                                                                                                                                                                           99WO-KR00555
                                                                                                                                                                                                                                                                                                                                                   /product= "LTS63Y mutant protein"
/transl_except= (pos:938..939, aa:Met)
/note= "This codon has an apparent 1 nucleotide
/note= "this codon which alters the reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
164..1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA.
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Chang J,

Yum

Chung

SXCCCCCCCCCCCCCCCCXXXFFFFXXRR

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alignment_block:
US-09-528-682-1 x AAS01505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cc are two novel detoxified and immunologically active proteins (LT mutants) derived by site-directed mutagenesis of the Al subunit of wild ctype LT. The substitution of Ser to Tyr at position 63 in LTS63v blocks cc NAD-binding. Deletion of Glu residues at positions 110 and 112 in ctide of the Al subunit of Cc wild type LT catalyses ADP ribosylation of Gs, a GTP-binding protein that cregulates camp levels. The resulting increase in cAMP is the cause of Cc diarrhoea in humans and animals e.g. pigs. The mucosal immunogenicities cof mutant heat-labile endotoxins LTS63v and LTdell110/112 were tested. CC froups of mice were immunised with LTS63v and LTdell110/112. The control CC groups received phosphate buffered saline (PBS) alone. The serum and CC mice immunised with LTS63v or LTdell110/112 contained high and CC comparable level of anti-LT antibodies in sera and faecal extracts compared with those immunised with wild-type LT. The LT mutants are CC useful as a vaccine for preventing and treating diarrhoea and as an antibody production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AAS01505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes for Escherichia coli heat-labile enterotoxin (LT) mutant LTS63Y. LTS63Y and LTdell110/112 (AAU00507)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-281524/29
P-PSDB; AAU00506.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adjuvant for antibody production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                     yGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyV 134
                                                                                                                 LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl
                                                                                                                                                                                                            yrIleTyrVallleAlaThrAlaProAsnMetPheAsnValAsnAspVal 100
                                                                                                                                                                                                                                                                                                   GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                lyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThrGlnThr
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                                                                                           TTAGGCGTATACAGCCCTCACCCATATGAACAGGAGGTTTCTGCGTTAGG
                                                                                                                                                                                       ATATATATGTTATAGCGACAGCACCAAATATGTTTAATGTTAATGATGTA
                                                                                                                                                                                                                                                                                AAGTGCTCACTTAGCAGGACAGTCTATATTATCAGGATATTCCACTTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGTTCCGGAGGTCTTATGCCCAGAGGGCATAATGAGTACTTCGATAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
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: 5.431
: 99.583
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seq_documentation_block:
ID AAQ23864 standard: |
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                                   The thermolabile toxin (LTh) gene sequence is derived from enterotoxigenic E. coli. An LTh-STla-STlb probe, wherein all all or part of the sequences of the three toxin genes represented in AAQ23864-66 are ligated to each other by T4DNA ligase, may be to for the detection of Vibrio cholerae and enterotoxigenic E.coli simultaneously in a simple way.

The method has the same sensitivity as the dangerous radio-isotope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     718
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                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                  Esherischia coli.
                                                                                                                                                                                                                                                                                                                                                                                          probe; detection;
                                                                                                                                                                                                                                                                                                                                                                                                        LTh; STla; STlb; thermolabile; heat-stable; E.coli; T4DNA ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ23864 standard; DNA; 1148
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                                                                                                                                                                                                                                  (KITA ) KITASATO RES
                                                                                                                                                                                                                                                                                      23-JUL-1990;
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                                                                                                                                                                     entero-toxigenic
                                                                                                                                                                                 and RNA probe -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTTAAGAGGCAGATATTTTCAGACTATCAGTCAGAGGTTGACATATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAGAATTCGGGATGAATTA
                                                                                                                                                                                                          1992-137930/17
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                                                                                                                                                                                                                                                                                                                                                                                                                                toxin (LTh)
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                                                                                                                                                                                                                                                            90JP-0194208
                                                                                                                                                                                                                                                                                    90JP-0194208
                                                                                                                                                                    for simultaneous E. coli
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                                      the dangerous radio-isotope
                                                                                                                                                                                 of Vibrio cholerae
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Sequence 1148 BP;

399

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205 C;

229 G;

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method

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alignment_block:
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Ratio: 5.383
Similarity: 100.000
snArgIleArgAspGluLeu 240
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|ACAGAATTCGGAATGAATTA 774
                                                       SValLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA 234
                                                                                                                                                                                            roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn 200
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                                                                                                                                                                                                                                                                                                                                                                        alIleAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyr 150
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                                                                                                                                 GluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLy
                                                                                                                                                                                                                                                                                                               ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh 167
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                                                                                                                  CACAAGGTTGTGGAAATTCATCAAGAACAATTACAGGTGATACTTGTAAT
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                                                                                                                                                                                                                                                                                                AGAAATCTGAATATAGCTCCGGCAGAGGATGGTTACAGATTAGCAGGTTT
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seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAA51106
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alignment_block:

Percent Similarity:

alignment_scores:

Quality: Ratio:

1287.00 5.362

Length: Gaps: Percent Identity:

240 0 98.333

100.000

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seq_documentation_block:
ID AAA51106 standard; cl
XX AAA51106;
XX AAA51106;
XX Plant-optimized E. cc
XX Plant-optimized E. cc
XX Heat-labile toxin; L1
KW Heat-labile toxin; L1
KW Heat-labile toxin; L1
KW Heat-labile toxin; L1
KW Adjuvant; anti-bacter
XX Escherichia coli.
CS Synthetic.
XX Synthetic.
XX Synthetic.
XX Synthetic.
XX Heat Lpeptide 3..55
FT Sig_peptide 57..7
FT CDS /*tag
FT Sig_peptide 57..7
FT Sig_peptide 57..7
FT AND WO200037609-A2.
XX WPI; 2000-442653/38.
PP SDB; AAY96646.
XX WPI; 2000-426646.
XX WPI; 2000-442653/38.
PP SDB; AAY96646.
XX W
                                                                                       This plant-codon optimized cDNA encodes a synthetic Escherichia coli
(heat-labile toxin (LT) A subunit (LT-A). The sequence contains
plant-preferred codons and eliminates sequence motifs associated with
spurious mRNA processing. A single codon insertion (GTG encoding valine)
was made to accomodate the creation of a NcoI restriction site around the
initiator methionine codon. Novel polynucleotides encode a mutant LT-A
(CT-A) polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit
(CT-A) polypeptide, which have reduced enzyme activity as compared to the
wild-type LT-A or CT-A polypeptide and where at least one of the codons
is altered to a plant preferred codon. The polypucleotide further
comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B
subunit (CT-B). The polypucleotides are useful for the transformation of
plant cells for the production of transgenic plants to produce edible
vaccines, especially oral vaccines in transgenic plants for the
prophylactic or therapeutic treatment against E. coli or V. cholerae. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-442653/38
P-PSDB; AAY96646.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 1; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BOYC-) BOYCE THOMPSON INST PLANT
(MASO/) MASON H S.
(ARNT/) ARNTZEN C J.
                                                                      polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anti-bacterial; ss.
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3..56
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57..779
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          225 A;
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             186 C;
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             T; 0 other;
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seq_documentation_block:
ID     AAA51147 standard; cf
     XX
     AC     AAA51147;
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     DT     26-SEP-2000 (first e
     XX
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                                                                                                                            /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2000.DAT: AAA51147
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alignment_block:

Percent Similarity:

100.000

Percent Identity:

Length:

one or

240 0 97.917

Quality: 1283.00 Ratio: 5.346

US-09-528-682-1 x AAA51147

alignment_scores:

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the initiator methionine codon. Novel polynucleotides encode a mutant LIT-A polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the prophylactic or therapeutic treatment against E. coll or V. cholerae. The mutant polypeptides are also useful as adjuvants. Note: This sequence does not appear in the specification. It was constructed from the wild type LT-A CNNA shown in AAA51106 which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This cDNA encodes a mutant S63K Escherichia coli heat-labile toxin (LT) A subunit (LT-A). The codon at nucleotide positions 246-248 was changed from the wild-type TCC to AAG which causes a change of serine to lysine in the mature protein at residue 63. The sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding valine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transformation of plant cells, useful in immunogenic compositions elicit immune responses in animals % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right
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(MASO/) MASON H S.
(ARNT/) ARNTZEN C J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides encoding LT-A or CT-A polypeptides for the
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          782 BP;
                                                                                                     Figure 1 of the specification.
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seq_documentation_block:
ID AAA51545 standard; cf
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AC AAA51545;
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C SEP-2000 (first e
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DE Plant-optimized E. co
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               Plant-optimized E. coli LT-A R72 mutant coding sequence
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| GCTTTGTGAGGTATGATGATGATGTGTCCACCAAGCTTAGCTTGAG
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alignment_scores:
                                                                        This cDNA encodes a mutant A72R Escherichia coli heat-labile toxin (LT) CC A subunit (LT-A). The nuclectides at position 273-274 were changed from the wild-type GC to AG which causes a change of alanine to arginine in CC the mature protein at residue 72. The sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to accomodate the creation of a NGOI restriction site around the codo codon entiator methionine codon. Novel polynucleotides encode a mutant LT-A collypeptide or a mutant vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further CC comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edble corphylactic or therapeutic treatment against E. coli or V. cholerae. CC more constructed from the wild type LT-A cDNA shown in AAA51106 which is constructed from the wild type LT-A cDNA shown in AAA51106 which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions elicit immune responses in animals
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P-PSDB; AAY96649.
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Synthetic.
                                                  Sequence 782 BP;
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alignment_block: US-09-528-682-1 x AAA51545

Percent Similarity:

Quality: Ratio:

: 1282.00 : 5.364 : 99.583

Percent

Gaps: Identity:

0 97.917

Align seg 1/1

to: AAA51545

from:

Н

to: 782

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seq_documentation_block:
ID AAA51544 standard; cI
XX
AC AAA51544;
XX
DT 26-SEP-2000 (first e
XX
DT Plant-optimized E. cc
XX
KW Heat-labile toxin; LI
KW adjuvant; anti-bacter
                                                                                                                                                                                          seq_name:
Heat-labile toxin; LT-A; LT-B; mutant;
adjuvant; anti-bacterial; R192G; ss.
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                                                                                                                                                                                                                                                                                  GGTGAAGAGGCAAATCTTCTCAGACTACCAATCAGAGGTGGACATCTACA
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                                                                                                                                                                                      /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2000.DAT: AAA51544
                                                                             (first entry)
                                                                                                                                            cDNA; 782
                transgenic plant; vaccine; oral;
                                                                                                                                                                                                                                                                                                                                                709
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alignment_block:
US-09-528-682-1 x AAA51544
                                                                                                                                                                   alignment_scores:
Align seg 1/1
                                                                          Percent Similarity:
                                                                                                                                                                                                         initiator methionine codon. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the prophylactic or therapeutic treatment against E. coli or V. cholerae. The mutant polypeptides are also useful as adjuvants.

Note: This sequence does not appear in the specification. It was constructed from the wild type LT-A CDNA shown in AAA51106 which is
                                                                                                                                                                                                                                                                                                                                                                                                         This cDNA encodes a mutant R192G Escherichia coli heat-labile toxin (L7 A subunit (LT-A). The nucleotide at position 631 was changed from the wild-type A to G which causes a change of arginine to glycine in the mature protein at residue 192. The sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to accommodate the creation of a NcoI restriction site around the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
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                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page -; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mason HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BOYC-) BOYCE THOMPSON INST PLANT RES
(MASO/) MASON H S.
(ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-1999;
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                                                                                                      Quality:
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                                                                                          Ratio:
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 to: AAA51544
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5.356
99.583
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from:
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0
97.917
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(II)

1 AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy

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seq_documentation_block:
ID AAS01506 standard; DN
XX
AC AAS01506;
XX
DT 29-AUG-2001 (first e
XX
DT 29-AUG-101 enterotox
KW Heat-labile enterotox
KW detoxified and immuno
KW endotoxin; diarrhoea;
XX
                                                                                                                               seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAS01506
        Heat-labile enterotoxin; LT; LTS63Y; LTdel110/112; mutant; detoxified and immunologically active protein; ADP-ribosylation; endotoxin; diarrhoea; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                snArgIleArgAspGluLeu 240
                                                                                                                                                                                                 sValLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA 234
                                                                                                                                                                                                                                                                 CACAAGGTTGTGGAGACTCCTCAGGGACCATCACAGGTGACACTTGCAAT
                                                                                                                                                                                                                                                                           roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn
                                                                                                                                                                                                                                                                                                     CCCACCAGACCACCAAGCCTGGAGGGAGGAGCCCTGGATCCACCATGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                             yGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl
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                                                                                                                                                    ATAGGATTAGGAATGAACTC 779
                                                                (first entry)
                                                                                                      DNA;
                                               enterotoxin (LT) mutant LTdel110/112
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                                                                                                      ВP
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                   GS;
                                                                                                                                                                                       alignment_block:
US-09-528-682-1 x
                                                                                                                                                           alignment_scores:
                                                                                 Align seg 1/1
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1 AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy

6

from: 1

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1508

AAS01506 AAS01506

17

sArgSerGlyGlyLeuMetProArgGlyHisAsnGluTyrPheAspArgG

34 4 267 Sequence 1508

BP;

506 A;

277

Ç 295

ر. و

430 T;

other;

that

Similarity:

Percent

Length: Gaps: Identity:

98

Quality: 1280.00 Ratio: 5.378 milarity: 99.167

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The present sequence encodes for Escherichia coli heat-labile centerotoxin (LT) mutant LTdell10/112. LTS63Y (ABU00506) and LTdell10/112 CC are two novel detoxified and immunologically active proteins (LT cutants) derived by site-directed mutagenesis of the Al subunit of wild type LT. The substitution of Ser to Tyr at position 63 in LTS63Y blocks (LT catalyses) Deletion of Glu residues at positions 110 and 112 in CC LTdell10/112 eliminate the enzymatic activity of LT. The Al subunit of CC wild type LT catalyses ADP-ribosylation of Gs. a CTP-binding protein that CC regulates CAMP levels. The resulting increase in cAMP is the cause of CC diarrhoea in humans and animals e.g. pigs. The mucosal immunogenicities CC of mutant heat-labile endotoxins LTS63Y and LTdell10/112 were tested. CC croups of mice were immunised with LTS63Y or LTdell10/112. The control CC groups received phosphate buffered saline (PBS) alone. The serum and CC mice immunised with LTS63Y or LTdell10/112 contained high and CC comparable level of anti-LT antibodies in sera and faceal extracts comparable level of anti-LT antibodies in sera and faceal extracts are useful as a vaccine for preventing and treating diarrhoea and as an cafiunant for antibody production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New detoxified mutants of Escherichia coli heat-labile enterotoxin useful as vaccine for preventing and treating diarrhoea, and as adfor antibody production \,\cdot\,
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adjuvant for antibody production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Page 45-46; 48pp;
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/transl_except= (pos:932..933,aa:Met)
/note= "This codon has an apparent 1 nucleotide
deletion which alters the reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
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164..1305
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seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:AAQ42768
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AAQ42768 standard;
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                                                                                                                                               E.coli heat labile toxin subunit A coding sequence
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                                                                                                                      enterotoxigenic bacteria; vaccine; immunogenic
                                                                                                                                                                             08-DEC-1993
                         mat_peptide
                                                                  Escherichia
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                                                                                                                                                                                                                                                                                                                                                                        sValLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA 234
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                                                                                                                                                                                                                                                                                                     ACAGAATTCGGGATGAATTA
                                                                                                                                                                                                                                                                                                                                                         AGTTAAGAGGCAGATATTTTCAGACTATCAGTCAGAGGTTGACATATATA
                                                                 coli.
                                                                                                       site-directed mutagenesis;
                                                                                                                                                                            (first entry)
                                     Location/Qualifiers
           /*tag=
                                                                                            activity;
                                                                                                                                                                                                                                                                                                      931
                                                                                            SS
                                                                                                       reduced
                                                                                                         toxicity;
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Ratio:
Percent Similarity:
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                                                                                                                                                                                          GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr
yGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyV
                                                                                                                                                                              GGCTTTGTCAGATATGATGACGGATATGTTTCCACTTCTCTTAGTTTGAG
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seq_documentation_block:
ID AAV81595 standard.
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Detoxified mutants of bacterial ADP-ribosylating toxins as parenteral adjuvants - useful to enhance humoral and cell-mediated immune responses in vertebrates when administered with selected antigen e.g. in disease treatment
                                                                                                     WPI; 1999-070064/06.
P-PSDB; AAW67772.
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21-MAR-1997;
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This sequence corresponds to the coding region for the A subunit of the

Disclosure; Fig 1A-B; 51pp; English

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alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E. coli heat labile toxin, an example of a bacterial ADP-ribosylating toxin. A mutant detoxified form of this protein is used in a parenters adjuvant composition, which comprises the detoxified protein, at least one selected antigen and optionally a pharmaceutically acceptable (optionally topical) vehicle. The adjuvant composition can be administered parenterally in conjunction with at least one antigen in methods to immunise vertebrate subjects. The adjuvant has the ability to enhance the humoral and cell-mediated immune responses elicited by
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                                                                                                yGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyV
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seq_documentation_block:
ID AAQ51317 standard;
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The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al. J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected tite-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to
                                                                                                            Claim 3;
                                                                                                                                            Immunogenic detoxified mutant cholera toxin and heat labile toxin - useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enterotoxigenic bacteria; vaccine; immu protomer A; site-directed mutagenesis; ADP-ribosyltransferase activity; ss.
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                                                                                                            Fig 2 and Page 46;
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                                                                                                      roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn
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sValLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA
                               CACAAGGTTGTGGAGATTCATCAAGAACAATCACAGGTGATACTTGTAAT
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ID AAQ51325 standard; DN
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AC AAQ51325;
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DT 08-DEC-1993 (first e
XX enterotoxigenic bacte
KW protomer A; site-dire
KW ADP-ribosyltransferas
XX Escherichia coli.
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Key protomer A; Site-dire
KW ADP-ribosyltransferas
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KPH Key Locat
FT misc_difference 328...
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US-09-528-682-1 x AAQ51325
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Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                     The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51325 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino acid numbering is based on the cholera toxin A subunit sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
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seq_documentation_block:
ID AAQ51326 standard; DN
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AC AAQ51326;
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DT 08-DEC-1993 (first e
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DT 08-DEC-1993 lfirst e
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Encodes Lys-114 E.col
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enterotoxigenic bacte
KW protomer A; site-dire

(first entry)

DNA; 711

Encodes Lys-114 E.coli heat labile

toxin subunit

LT-A;

enterotoxigenic bacteria; vaccine; immunogenic detoxified protomer A; site-directed mutagenesis; reduced toxicity;

seq_name:

/SIDS5/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:AAQ51326

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                                                                                                                                                                         CCCACCGGATCACCAAGCTTGGAGAGAAGAACCCTGGATTCATCATGCAC
                                                                                                                                                                                     eProProAspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCTTTGTCAGATATGATGACGGATATGTTTCCACTTCTCTTAGTTTGAG
                                           AGTTAAGAGGCAGATATTTTCAGACTATCAGTCAGAGGTTGACATATATA
ACAGAATTCGGGATGAATTA
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alignment_block:
US-09-528-682-1 x AAQ51326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic detoxified mutant cholera toxin and heat labile toxin - useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
 198
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                                                                   GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr
                                                                                                                         lyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThrGlnThr
                                                                                                                                                                                 sArgSerGlyGlyLeuMetProArgGlyHisAsnGluTyrPheAspArgG
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                                                                                                                                                                                                                                                                                                                                                   Similarity:
                                                                                                            GAACTCAAATGAATATTAATCTTTATGATCACGCGAGAGGAACACAAACC
                                                    GGCTTTGTCAGATATGATGACGGATATGTTTCCACTTCTCTTAGTTTGAG
                                                                                                                                                                    ACGTTTCCGGAGTCTTATGCCCAGAGGT...AATGAGTACTTCGATAGAG
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seq_documentation_block:
ID AAQ51316 standard; DNA; 711
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                                                                                                                                                               Escherichia coli
                                                                                                                                                                                                      enterotoxigenic bacteria; vaccine; immunogenic
                                                                                                                                                                                                                                                                     AAQ51316;
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                                                30-DEC-1992;
                                                                     08-JUL-1993.
                                                                                        W09313202-A
                                                                                                                                  misc_difference
                                                                                                                                                                                   ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                               protomer A;
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        (BIOC-) BIOCINE SCLAVO SPA
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                                                                                                                                                                                               site-directed mutagenesis; reduced
                                                                                                                                                                                                                                               (first entry)
                             91IT-0MI3513
                                                92WO-EP03016
                                                                                                                                 Location/Qualifiers 153..155
                                                                                                             /note= "wild-type GTC(Val) mutated
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alignment_scores:
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ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh
                                                                                      alIleAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyr
                                                                                                                                                                                                                                 ### ATTAGCGTATACAGCCCTCACCCATATGAACAGGAGGTTTCTGCGTTAGG
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                                                             TGATTGATGAACGATTACATCGTAACAGGGAATATAGAGACCGGTATTAC
                                                                                                                                               TGGAATACCATATTCTCAGATATATGGATGGTATCGTGTTAATTTTGGTG
                                                                                                                                                                   yGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyV 134
                                                                                                                                                                                                                                                                         LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl 117
                                                                                                                                                                                                                                                                                                                   TATATATCGTTATAGCA.....AATATGTTTAATGTTAATGATGTA
                                                                                                                                                                                                                                                                                                                                                                                                         AAGTGCTCACTTAGCAGGACAGTATATTATCAGGATATTCACTTACTA
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Ratio: 5.189
milarity: 94.583
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seq_documentation_block:
ID AAQ51319 standard;
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                                                                                                      Immunogenic detoxified mutant cholera toxin and heat labile - useful as vaccines against infection by Vibrio cholerae ar enterotoxin producing Escherichia coli
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protomer A; site-directed mutagenesis; reduced
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                                                                                    Claim 3; Fig 2 and Page 46; 60pp; English.
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                                                                                                                                                                          Domenighini M,
                                                                                                                                                                                            (BIOC-) BIOCINE
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|CACAAGGTTGTGGAGATTCATCAAGAACAATCACAGGTGATACTTGTAAT
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The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected t site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51319 is a combination of the wild-type coding sequence and the mutagenic

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US-09-528-682-1 x AAQ51319
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                                                                   eProProAspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaP 184
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                                                                                                                     CACAAGGTTGTGGAGATTCATCAAGAACAATCACAGGTGATACTTGTAAT
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Ratio: 5.189
milarity: 94.583
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seq_documentation_block:
ID AAQ51315 standard; DN
AC AAQ51315;
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XX enterotoxigenic bacte
KW enterotoxigenic bacte
KW protomer A; site-dire
KW ADP-ribosyltransferas
OS Escherichia coli.
XX Key protomer A; Docat
FH Key Locat
FT misc_difference 153.
XX Key ADP-ribosyltransferas
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ADP-ribosyltransferase activity; ss.
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Ratio: 5.185
milarity: 94.583
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seq_documentation_block:
ID AAQ51318 standard; DN
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AC AAQ51318;
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Encodes Lys-97 E.col1
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KW enterotoxigenic bacte
KW protomer A; site-dire
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OS Escherichia coli.
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protomer A; site-directed mutagenesis; reduced
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                                toxicity;
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eProProAspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaP

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                                                         GluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLy
                                                                                        TATATATCGTTATAGCA.....
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         sValLysargGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA
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                                            TGGAATACCATATTCTCAGATATATGGATGGTATCGTGTTAATTTTGGTG
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seq_name:

/SIDS5/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:AAQ51324

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seq_documentation_block:
ID AAQ51324 standard; DN
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AC AAQ51324;
XX AAQ51324;
XX O8-DEC-1993 (first e
XX enterotoxigenic bacte
KW enterotoxigenic bacte
KW protomer A; site-dire
KW ADP-ribosyltransferas
OS Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic detoxified mutant cholera toxin and heat labile t - useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                                                                     148
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Immunogenic detoxified

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5.172
94.583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent
                                                                                                                                                                                                                                                                                                                                                                                                     AATATGTTTAATGTTAATGATGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by Vibrio cholerae
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92.917
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seq_documentation_block:
ID AAQ51322 standard;
seq_name:
                               The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected toxite-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51322 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino primer sequence used to introduce the preferred mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          539
                                                                                                                                                                 Claim 3;
                                                                                                                                                                                          enterotoxin
                                                                                                                                                                                                                                                                                  Domenighini M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protomer A; site-directed mutagenesis; reduced
ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ51322;
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                      acid numbering is based on the cholera
                                                                                                                                                                                       Immunogenic detoxified mutant cholera toxin and l
- useful as vaccines against infection by Vibrio
enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                            30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                    08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enterotoxigenic bacteria; vaccine; immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Encodes Asp-104 E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                                          (BIOC-) BIOCINE SCLAVO SPA.
                                                                                                                                                                                                                                                                                                                                                                                                            W09313202-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     snArgIleArgAspGluLeu 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAGAATTCGGGATGAATTA
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                                                                                                                                                                                                                                            AAR44021
                                                                                                                                                                 Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coli.
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                                                                                                                                                                                                                                                                                  Hol W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 298..300
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                                                                                                                                                                                                                                                                                  Pizza
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                                                                                                                                                                                                                                                                                  Rappuoli
                       COXID
                       A subunit sequence)
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o cholerae ar
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                                                                                                                                                                                                       le toxin
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Sequence 711 BP;

234 A; 122 C;

157

<u>و</u> 198

T; 0 other;

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alignment_block:
US-09-528-682-1 x AAQ51322
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Quality:
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||||||||||||||||||||||||
|ACAGAATTCGGGATGAATTA 708
                                                     sValLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA 234
                                                                                              GluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLy
                                                                                                                                                                                                                                                                                                                                                                                                 yrIleTyrVallleAlaThrAlaProAsnMetPheAsnValAsnAspVal 100
||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                            gSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyTyrSerThrTyrT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr
                                                                                   CACAAGGTTGTGGAGATTCATCAAGAACAATCACAGGTGATACTTGTAAT
                                                                                                                                        roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn
                                                                                                                                                                     CCCACCGGATCACCAAGCTTGGAGAAGAACCCTGGATTCATCATGCAC
                                                                                                                                                                                 eProProAspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCTTTGTCAGATATGATGACGGATATGTTTCCACTTCTCTTAGTTTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity:
                                          AGTTAAGAGGCAGATATTTCAGACTATCAGTCAGAGGTTGACATATATA
                                                                                                                                                                                                                                                                                                                                                                                     TATATATCGTTATAGCA.....AATATGTTTAATGTTAATGATGTA
                                                                                                                                                                                                                                                                                                                                                                                                                               AAGTGCTCACTTAGCAGGACAGTATATTATTATCAGGATATTCACTTACTA
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5.167
94.583
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Gaps:
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seq_documentation_block:

/SIDS5/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:AAQ46318

51

GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr

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alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                           Align seg 1/1 to: AAQ46318
                                                                                                                                                                             Percent Similarity:
                                                                                                                                              US-09-528-682-1 x AAQ46318
                                                                                                                                                                                                                                                           This sequence encodes the A subunit of the cholera toxin (CT-A) of Vibrio cholerae. The sequence was published by Mekalanos et al., Nature 306, 551 (1983). Mutations at selected positions within this sequence have been found to reduce toxicity (see AAOS1327-Q51334). The invention relates to immunogenic, detoxified CT-A proteins and their use in vaccines to protect against cholera.
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1993-227320/28.
P-PSDB; AAR38729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic detoxified CT-A; cholera vaccine; adenylate cyclase; protomer A; site-directed mutagenesis; reduced toxicity; ADP-ribosyltransferase activity; ss.
 101
                                                                                                                                                                                                                                          Sequence 723 BP;
                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                           enterotoxin
                                                                                                                                                                                                                                                                                                                                                                    Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                                                                                                                                                                  Domenighini M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-DEC-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cholera toxin
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                    34
                                         51
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                                                                                 cholerae.
                                                                                                                                                                                                                                                                                                                                                           producing Escherichia coli
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4.814
94.167
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1..720
/*tag=_a
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                                                                                                                                                                                                                                          227 A;
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                                                                                                                           from:
                                                                                                                                                                            Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                          C; 163 G;
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6
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                                                                                                                                                                                                                                          208 T; 0 other;
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0
81.667
                    50
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seq_documentation_block:
ID AAV81596 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name:
                                                                                                                                                                                                 A subunit; heat labile toxin; ADP-ribosylation; mutant; detoxification; parenteral adjuvant; antigen; antigen; immunisation; humoral response; cell-mediated immune response; virus; bacterium; parasite; fungus; tumour; allergen; pathogen; AIDS; autoimmune disease; cancer; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601
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                                                                                                                                                                                 systemic
                                                                                                                                                                                                                                                                                              Cholera toxin gene.
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18-MAR-1998;
                                  19-MAR-1998;
                                                                                                          W09842375-A1
                                                                                                                                               Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                   11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                       AAV81596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLy 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eProProAspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTAACTTAGATATTGCTCCAGCAGCAGATGGTTATGGATTGGCAGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alIleAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyr 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCCGGGTTGTGGGAATGCTCCAAGATCATCGATCAGTAATACTTGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATATATATGTTATAGCCACTGCACCCAACATGTTTAACGTTAATGATGTA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyTyrSerThrTyrT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:AAV81596
                                                                                                                                                                                 lupus
                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                 erythematosus;
                                  98WO-US05454.
                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
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Sequence 723

BP;

227 A; 125

C; 163

G; 208

T; 0 other;

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immunise vertebrate subjects. The adjuvant has the ability to enhance the humoral and cell-mediated immune responses elicited by the antigen (e.g. by making the antigen more strongly immunogenic or necessitating fewer/lower antigen doses). It can be administered prior/subsequent to the antigen, and is preferably administered within a short space of time to the same site; it can also be administered in isolation from antigens as a boost following systemic or mucosal antigen administration. Most preferably, the adjuvant is co-administered with the antigen in the compositions and a pharmaceutically acceptable carrier. The antigen may be derived from viruses, bacteria, parasites and fungi or may be tumour antigens, self-antigens and allergens. The compositions are therefore useful in the treatment and prevention of e.g. viral diseases, allergic manifestations, diseases caused by pathogens (e.g. bacteria or parasites).
                                              Erythematosus), Alzheimer's disease and cancers. The adjuvant cabe used to prepare antibodies against selected antigen(s), useful e.g. for diagnostic purposes or for antigen purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    selected antigen and optionally a pharmaceutically acceptable (optionally topical) vehicle. The adjuvant composition can be administered parenterally in conjunction with at least one antigen in methods to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutant detoxified form of this protein is used in a parenteral adjuvant composition, which comprises the detoxified protein, at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence corresponds to the coding region for the A subunit of cholera toxin, an example of a bacterial ADP-ribosylating toxin. A mutant detoxified form of this protein is used in a parenteral adjunction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antigen e.g. in disease treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detoxified mutants of bacterial ADP-ribosylating toxins as parenteral adjuvants - useful to enhance humoral and cell-mediated immune responses in vertebrates when administered with selected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-1997;
                                                                                                                            parasites), AIDS, autoimmune diseases (e.g. Systemic Lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1A-B; 5lpp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barchfeld G,
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                                                                                                    The adjuvant can also
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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                                                                                                                                                                                              51 GCAGTCAGGTGGTCTTATGCCAAGAGGACAGAGTGAGTACTTTGACCGAG
                                                                                                                                                                                                                                                                              1 AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy
                                                                                 GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr
                                                                                                                                                lyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThrGlnThr
                                                                                                                                                                                                                sArgSerGlyGlyLeuMetProArgGlyHisAsnGluTyrPheAspArgG
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AAGTGCCCACTTAGTGGGTCAAACTATATTGTCTGGTCATTCTACTTATT
                                                                                                                           GTACTCAAATGAATATCAACCTTTATGATCATGCAAGAGGAACTCAGACG
                                                                                                                                                                                                                                                              AATGATGATAAGTTATATCGGGCAGATTCTAGACCTCCTGATGAAATAAA
                              gSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyTyrSerThrTyrT
                                                                GGATTTGTTAGGCACGATGATGGATATGTTTCCACCTCAATTAGTTTGAG
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Percent Identity:
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seq_documentation_block:
ID AAA51157 standard; cD
XX AAA51157;
AC AAA51157;
XX 26-SEP-2000 (first e
XX Plant-optimized v. ch
XX Heat-labile toxin; CT
KW Heat-labile toxin; CT
KW adjuvant; anti-bacter
XX Vibrio cholerae.
OS Vibrio cholerae.
Synthetic.
XX Vibrio cholerae.
YX Vibrio cholerae.
YX Vibrio cholerae.
YX Vibrio cholerae.
XX Vibrio cholerae.
XX Vibrio cholerae.
XX Vibrio cholerae.
XX PT CDS
Y*tag
FT CDS
Y*tag
FT CDS
Y*tag
FT Z2-DEC-1999; 99WO-L
XX Z2-DEC-1999; 99WO-L
XX Z2-DEC-1998; 98US-L
XX CBOYC-) BOYCE THOMPSC
PA (MASON H S.
PA (ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAA51157
                                                                                                                                                                                                                                                                                                                                  adjuvant; anti-bacterial;
                                                                                                                                                                                                                                                                                                                                                                              Plant-optimized V. cholerae toxin A subunit coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234
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                                                                                                                                                                                                                                                                                                                                             Heat-labile toxin; CT-A; CT-B; mutant; transgenic plant; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                     98US-0113507
                                                                                                    99WO-US30747
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/product=
                                                                                                                                                                                                                                   Location/Qualifiers
1..777
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XX Mason HS, Arntzen CJ;
XX PI; 2000-442653/38.

DR WPI; 2000-442653/38.

DR WPI; 2000-442653.

XX New polynucleotides encoding LT-A or CT-A polypeptides for the ransformation of plant cells, useful in immunogenic compositions to PT elicit immune responses in animals

XX Disclosure; Fig 4A; 103pp; English.

XX Conjuncted to CT, A subunit (CT-A), polypeptide or a mutant v. Cholerae cholera toxin (LT) compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide of turnber comprises a nucleic acid sequence encoding LT B subunit (CT-B). The polynucleotides are useful for the transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants to CT or the prophylactic or therapeutic treatment against E. coli or V. Cholerae. The mutant polypeptides are also useful as adjuvants.

XX Sequence 777 BP; 209 A; 174 C; 191 G; 203 T; 0 other;
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alignment_scores:
Quality: 1088.00
Ratio: 4.814
Percent Similarity: 94.167
Record Reco

alignment_block: US-09-528-682-1 x AAA51157

Align seg 1/1 to: AAA51157 from: 1 to: 777

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405
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                                                                                                                              305
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alIleAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyr 150
                                                                                                                                                                              LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl
                                                                                                                             yrIleTyrValIleAlaThrAlaProAsnMetPheAsnValAsnAspVal
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                          TGGAATCCCATACTCCCAAATCTATGGATGGTATAGGGTGCACTTTGGAG
                                                                             TTGGGAGCATACAGCCCTCACCCAGATGAGCAAGAGGTGTCTGCTTTGGG
                                                                                                                                                                                                                                   GGATTTGTGAGGCATGATGATGGATATGTGTCCACCTCCATTAGCTTGAG
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seq_documentation_block:
ID AAN30169 standard; DNA; 1148
                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:AAN30169
The for
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                            Claim
                                           DNA sequence transforming
                                                                       WPI; 1983-834665/49.
                                                                                         Harford N,
                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                            Vibrio cholerae
                                                                                                                                                                                                                                                                                                              Vaccine;
                                                                                                                                                                                                                                                                                                                              Sequence of pRIT 18014 encoding sub-unit A and
                                                                                                                                                                                                                                                                                                                                                                  AAN30169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                234
                                                                                                          (SMIK ) SMITH KLINE-RIT
                                                                                                                             24-MAY-1982;
                                                                                                                                             23-MAY-1983;
                                                                                                                                                                30-NOV-1983
                                                                                                                                                                                 EP95452-A.
                                                                                                                                                                                                                                                                                                                                                25-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                             inventors claim a sequence contg. at least one fragment all or part of sub-units A and B of cholera toxin. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                eProProAspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAAAGACCCAATCTTTGGGTGTGAAGTTCCTTGATGAGTACCAATCTAA
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                           2,
                         Page 27-28; 46pp; French.
                                                                                                                                                                                                                                                                                                             cholera; subunit A;
                                                                                        Dewilde
                                           coding for cholera toxin sub units host cells, useful in vaccine produ
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                            82US-0381083
                                                                                                                                              83EP-0091416
                                                                                                                                                                                                                            /label= F1
/note= "claimed
774..1148
                                                                                                                                                                                                           /label=
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1..777
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coding
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence and two fragments (F1 and F2) are listed in the specification. Also new are recombinant DNA molecules conty. the specences (spec. pRIT 18014 conty. the whole sequence; pRIT 1804 conty. F1 and pRIT 10810 conty. F2) and transformed host cells (E. coli ATCC 39052 conty. the whole sequence, ATCC 39053 conty. and ATCC 39051 conty. F2).
                            201
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              GluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLy
                                                                                                                                eProProAspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaP
                                                                                                                                                                                           ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh
                                                                                                                                                                                                                                                                                                                    yGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyV
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GAAAAAACCCAAAGTCTAGGTGTAAAATTCCTTGACGAATACCAATCTAA
                                                                                                                                                                                                                                          TGGGATTCCATACTCCCAAATATATGGATGGTATCGAGTTCATTTTGGGG
                                                                                                                                                                                                                                                                                                                                                                TTAGGGGCATACAGTCCTCATCCAGATGAACAAGAAGTTTCTGCTTTAGG
                                                         CGCCGGGTTGTGGGAATGCTCCAAGATCATCGATGAGTAATACTTGCGAT
                                                                                    roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn
                                                                                                                     CCCTCCGGAGCATAGAGCTTGGAGGGAAGAGCCGTGGATTCATCATGCAC
                                                                                                                                                                                AGTAACTTAGATATTGCTCCAGCAGCAGGTTATGGATTGGCAGGTTT
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sValLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA

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seq_documentation_block:
ID AAI67270 standard: |
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The invention provides a chimeric molecule that comprises a first subunit which is mutated A subunit of first enterotoxin and a second non-mutated subunit from a second enterotoxin which is different from the natural enterotoxin which has been mutated to provide A subunit. A composition of matter comprising the chimeric molecule in a pharmaceutically acceptable carrier is useful for obtaining enhanced immune response of an organism to an antigen by administering it to the antigen. The chimeric molecule is useful to provide specific immune response to a particular enterotoxin, as adjuvants for use with unrelated vaccines, and to customize adjuvants to direct production of cell-mediated or humoral immuneity. The present sequence represents the DNA sequence cholera toxin A and B subunits.
                                                                                                                                                                                                                                                                                                                                               Chimeric molecule useful as adjuvant for cell-mediated/humoral immunity comprises first mutated A subunit of first enterotoxin and second non-mutated subunit from second enterotoxin different from natural
                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB;
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1699..2056
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/note= "AAG65991"
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854 84 804 67 50 704 34 654 17

754

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Align seg 1/1

to:

AAA51159

from:

_ ţo: 777

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seq_documentation_block:
ID AAA51159 standard;
alignment_block:
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                                                                                                                                          This plant-codon optimized cDNA encodes a mutant synthetic CC Vibrio cholerae cholera toxin (CT) A subunit (CT-A) having a A72R CC substitution. The sequence had no CG cryptic signal sequence and no CG (potential methylation sites) sequences. Novel polynucleotides encode a mutant Escherichia coli heat-labile toxin (LT) subunit A (LT-A) CC polypeptide or a mutant V. cholerae cholera toxin (CT) A subunit (CT-A) CC polypeptide, which have reduced enzyme activity as compared to the CC wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further CC comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of CC vaccines, especially oral vaccines in transgenic plants for the production of transgenic plants for the prophylactic or therapeutic treatment against E. coli or V. cholerae. The mutant polypeptides are also useful as adjuvants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAA51159
                            Percent
                                                                                                                                                                                                                                                                                                                                                                                           Claim 15; Fig 4C; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding LT-A or CT-A polypeptides for
transformation of plant cells, useful in immunogenic compos
elicit immune responses in animals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heat-labile toxin; CT-A; CT-B; mutant; transgenic plant; vaccine; oral; adjuvant; anti-bacterial; A72R; ss.
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                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mason
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BOYC-) BOYCE THOMPSON INST PLANT RES. (MASO/) MASON H S. (ARNT/) ARNTZEN C J.
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                            Similarity:
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US-09-528-682-1 x AAA51159

Cholera toxin Al fragment.

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seq_documentation_block:
ID AAQ12710 standard; DN
XX
AC AAQ12710;
XX
DT 08-OCT-1991 (first e
XX
DE Cholera toxin A1 frag
XX
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alignment_scores:
Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                     Hybrid molecules are produced by covalently linking (1) a portion (A) of the binding domain of a cell-binding ligand, allowing binding of the mol. to an animal cell; (2) a portion (B) of a translocation domain of a protein able to translocate (C) across the cell cytoplamic membrane, and and (3) a portion (C) which is to be introduced into the cell. (A) is derived from a steroid or polypeptide hormone, a single-chain analogue of a monoclonal antibody able to bind an antigen expressed on the cell surface, or a polypeptide toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hybrid; fusion; membrane translocation; binding region; HIV; infection; toxin; steroid; hormone; monoclonal antibody; antigen; diphtheria; exotoxin; phenylketonuria; cholera; interleukin; IL-2; protease; epidermal growth factor; ricin; tetanus; hexosaminidase; Shiga-like toxin A; ligand; insulin; nuclease; ss.
                                                                                                                                                                                                     Specified examples are CT-A/DT-B'/IL-2, SLTA/DT-B'/IL-2, ricin A/DT-B'/IL-2, hydroxylase-DT-B' or their biologically active mutants. (CT-A-cholera toxin, DT-B'-truncated diphtheria toxin, SLTA-Shiga-like toxin A; HIVP-BP-HIV protease binding
                                                                                                                                                                                                                                                                                         (A) may be derived from insulin, interleukins epidermal growth factor. Suitable enzymes in (C) include cholera toxin
                                                                                                                                                                                                                                                                                                                                           analogue of a monoclonal antibody on the cell surface, or a polypept (B) is derived from a toxin (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hybrid molecules for targetting chemical entity to cell - have membrane trans-locating and cell binding-regions and used to treat HIV infection, genetic enzyme-deficiency disorders etc.
                                                                                                                                                                                                                                                                                  sequence),
                                                                                                                                                                                                                                                                                                                                  exotoxin
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22-DEC-1989;
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                                                              -528-682-1
AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy
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                                                                                                                                                                                                                                                                                ricin, tetanus toxin, hexosamininidase A, protease,
                                                           x AAQ12710
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89US-0456095.
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seq_documentation_block:
ID AAT91636 standard; DNA;
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            interleukin-2;
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                                                           Vibrio cholerae toxin
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                                                                                                                                                                                             ATAGAATTAAGGATGAATTA
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                                                                                 entry)
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Cholera toxin A1; hybrid protein; cell delivery; cell binding ligand; translocation domain; dipht
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| AAGTGCCCACTTAGTGGGTCAAACTATATTGTCTGGTCATTCTACTTATT
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leukaemia; therapy;
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                diphtheria toxin
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alignment_block:
US-09-528-682-1 x AAT91636
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                                                                                                                                                                                                                                                                              This sequence comprises the Vibrio cholerae gene that encodes cholera toxin (see AAW25785). DNA encoding an enzymatically active Al fragment of the cholera toxin was used to construct a cholera toxin Al-diphtheria toxin B'-interleukin-2 (CTA-DTB-IL2) gene that toxin Al-diphtheria toxin B'-interleukin-2 (CTA-DTB-IL2) gene that was expressed in E. coli. The hybrid protein can be isolated and used e.g. as an adjunct to treatment with DTB-IL2 hybrid, which targets the cell-killing ability of diphtheria toxin to cells bearing the IL2 receptor, such as certain leukaemic T cells. Prior application of the CTA-DTB-IL2 hybrid alleviates the problem of endogenous IL2 competing with DTB-IL2 hybrid for IL2 receptors on T cells. Claimed hybrid proteins comprise a translocation domain and a cell binding domain from e.g. a hormone, used for the delivery of agents (e.g. therapeutic genes, toxins, detectable labels) into cells. The use of a translocation mechanism ensures that the hybrid will be effective in relatively low doses, since a high proportion of the substance of interest will be taken into the targeted cells. The hybrid molecules can be manufactured as a single hybrid recombinant protein, permitting composition, consistency, and the precise control of
                                                              Align seg 1/1 to: AAT91636
                                                                                                                                            Percent Similarity:
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07-JUN-1985;
22-DEC-1989;
14-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New hybrid molecules for delivery of agents binding domain of a cell binding ligand and translocation domain of a protein
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                                                                                                                                                                                                                                         Sequence 780
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P-PSDB; AAW25785.
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              AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy
AATGATGATAAGTTATATCGGGCAGATTCTAGACCTCCTGATGAAATAAA
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89US-0456095.
90US-0538276.
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85US-0726808.
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1..777
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/transl_except= (pos:616..618, aa:Ala)
                                                                                                                                                                                                                                         243 A;
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104
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cholerae Al fragment toxin gene.

(first entry)

Recombinant; hybrid; binding domain; ligand; animal cell; diphtheria; translocation domain; botulinum; neurotoxin; ricin; cholera; tetanus; shiga-like toxin; pertussis; translocation; cytoplasmic membrane; HIV cytosol; therapy; genetic deficiency disease; enzyme; co-factor; pois adipocyte; cancer; virus; infection; antibody; ss.

poison;

documentation_block:

standard;

DNA; 780

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seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:AAZ30661
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                                            234 snArgIleArgAspGluLeu
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GCAGTCAGGTGGTCTTATGCCAAGAGGACAGAGTCAGTACTTTGACCGAG
                                                                                                                                                                                                                                                ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh
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                                                                                                sValLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA
                                                                                                                                                     GluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLy
                                                                                                                                                                                                           roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn
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                                                                                                                                       GAAAAAACCCAAAGTCTAGGTGTAAAATTCCTTGACGAATACCAATCTAA
                                                                                                                                                                                                                                                                                                                                                           TTAGGGGCATACAGTCCTCATCCAGATGAACAAGAAGTTTCTGCTTTAGG
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                             ATAGAATTAAGGATGAATTA
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Vibrio cholerae

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alignment_block:
US-09-528-682-1 x AAZ30661
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Quality:
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                                                                                                                              Align seg
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27-JUN-1991;
25-APR-1985;
07-JUN-1985;
22-DEC-1989;
14-JUN-1990;
   105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant DNA molecule encoding the treatment of Aids and genetic
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P-PSDB; AAY55890.
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                                                           GCAGTCAGGTGGTCTTATGCCAAGAGGACAGAGTCAGTACTTTGACCGAG
                 sArgSerGlyGlyLeuMetProArgGlyHisAsnGluTyrPheAspArgG
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Similarity:
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84US-0618199.
91US-0722484.
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90US-0538276
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seq_documentation_block:
ID AAZ90017 standard; DN
XX
AC AAZ90017;
XX
DT 05-MAY-2000 (first e
XX
DT Vibrio cholerae toxin
XX
Cholera toxin; hybric
KW genetic deficiency di
KW adipocyte; enzyme del
XX
PN Vibrio cholerae.
XX
PN US6022950-A.
XX
OS-FEB-2000.
                                                                                                                                                                                                                                                                               seq_name: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAZ90017
                                                                                     Cholera toxin; hybrid protein; translocation domain; cell binding domain; genetic deficiency disease; cell targetting; cell destruction; cancer; adipocyte; enzyme delivery; anti-viral; HIV; ds.
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| AGTAACTTAGATATTGCTCCAGCAGCAGATGGTTATGGATTGGCAGGTTT
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alignment_scores:
Quality: 1085.00
Ratio: 4.801
~~~~1arity: 94.167
                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the Vibrio cholerae toxin gene. The toxin can CC be included in the hybrid protein of the invention and used to destroy or CC modify the cell that the hybrid protein is trangeted to. The hybrid CC protein comprises a first part which is a portion of the binding domain CC of a cell-binding ligand, effective to cause the hybrid molecule to bind CC to a cell of an animal. The second part comprises a portion of a CC translocation domain of a naturally occurring protein (e.g. the CC translocation domain of diphtheria toxin) the second part translocates CC the third part across the cytoplasmic membrane and into the cytosol of CC the cell. The third part comprises a chemical entity to be introduced into the cell, where each of the first and third part is non-native with CC respect to naturally occurring protein, and the covalent bond attaching CC the second and third part is cleavable. The toxin encoded by the present CC ell binding domain binds to a specific cell membrane into the cytosol. CC The third part of the protein, linked to the translocation domain through a cleavable bond, can then carry out its function. The hybrid molecules are useful for treating genetic deficiency diseases by delivering to CC cellular levels of a particular enzyme or a scarce precursor or cofactor, to charter toxins or other noisons to destroy particular cells (such as
                                                                                                                                                                                              Align seg 1/1 to: AAZ90017
                                                                                                                                                                                                                                    US-09-528-682-1 x AAZ90017
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07-JUN-1985;
22-DEC-1989;
14-JUN-1990;
04-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New two-part hybrid protein comprising a translocation domain and a cell-binding domain, for treating genetic deficiency diseases, cancer and {\it HIV} infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murphy JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1984;
27-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              to direct toxins or other poisons to destroy particular cells (such at adipocytes, cancer cells, or virus-infected cells), and to counteract viral infections such as HIV by introducing into appropriate cells antibodies to viral proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 5; 32pp; English.
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P-PSDB; AAY78590.
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                                        GCAGTCAGGTGGTCTTATGCCAAGAGGACAGAGTCAGTACTTTGACCGAG
                                                                                                                  lyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThrGlnThr
                                                                            SArgSerGlyGlyLeuMetProArgGlyHisAsnGluTyrPheAspArgG 34
                                                                                                                                                        AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy
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85US-0742554.
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91US-0722484
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FTTH KWW KW XXX
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ID AAQ51328 standard; i
                                                                                                                                                                                                                                                                                                                                  seq_name:
                                                                                                                                                                                              Encodes Lys-63 cholera toxin subunit
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                                                          misc_difference
                                                                                                      Vibrio
                                                                                                                                                  Immunogenic detoxified CT-A; cholera vaccine; adenylate cyclase;
protomer A; site-directed mutagenesis; reduced toxicity;
                                                                                                                                    ADP-ribosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                  ATAGAATTAAGGATGAATTA
                                                                                                                                                                                                                                                                                                                                 /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:AAQ51328
                                                                                                      cholerae
                                                                                                                                                                                                                            (first
                                                        Location/Qualifiers 187..189
                          /note= "wild-type TCA(Ser) mutated to AAG(Lys)"
                                                                                                                                                                                                                            entry)
                                                                                                                                    activity;
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alignment_block:
US-09-528-682-1 x AAQ51328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
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|CAGTCAGGTGGTCTTATGCCAAGAGGACAGAGTGAGTACTTTGACCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity:
           yrIleTyrValIleAlaThrAlaProAsnMetPheAsnValAsnAspVal
                                                                                                                                           GTACTCAAATGAATATCAACCTTTATGATCATGCAAGAGGAACTCAGACG
TGGGATTCCATACTCCCAAATATATGGATGGTATCGAGTTCATTTTGGGG
                                              TTAGGGGCATACAGTCCTCATCCAGATGAACAAGAAGTTTCTGCTTTAGG
                                                        LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl
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Ratio: 4.796
nilarity: 94.167
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seq_documentation_block:
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                  Claim 3; Fig 2 and Page 48; 60pp; English.
                                       Immunogenic detoxified mutant cholera toxin and I useful as vaccines against infection by Vibrio enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ51334;
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ51334 standard; DNA;
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                                                                                     WPI; 1993-227320/28.
P-PSDB; AAR44033.
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                                                                                                                      Domenighini M,
                                                                                                                                           (BIOC-) BIOCINE
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protomer A; site-directed mutagenesis; reduced toxicity;
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                                                                                                                     Hol
                                                                                                                                            SCLAVO
                                                                                                                                                                                                                                                                           Location/Qualifiers 340..342
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The wild-type sequence coding for the A subunit

of the cholera

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alignment_scores:
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                                                                                                                               allleAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyr 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy
GAAAAAACCCAAAGTCTAGGTGTAAAATTCCTTGACGAATACCAATCTAA
             GluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLy
                                                                                                                                                                                                                   ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh
                                                                                                                                                                                                                                                                                                                                     TGGGATTCCATACTCCCAAATATATGGATGGTATCGAGTTCATTTTGGGG
                                                                                                                                                                                                                                                                                                                                                        yGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATATATATGTTATAGCCACTGCACCCAACATGTTTAACGTTAATGATGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yrIleTyrValIleAlaThrAlaProAsnMetPheAsnValAsnAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGTGCCCACTTAGTGGGTCAAACTATATTGTCTGGTCATTCTACTTATT
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                                                                CGCCGGGTTGTGGGAATGCTCCAAGATCATCGATCAGTAATACTTGCGAT
                                                                                                roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn
                                                                                                                                                                                                   AGTAACTTAGATATTGCTCCAGCAGCAGATGGTTATGGATTGGCAGGTTT
                                                                                                                                                                                                                                                                      TTAGGGGCATACAGTCCTCATCCAGATGAACAAGAAGTTGAAGCTTTAGG
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seq_documentation_block:
ID AAA51158 standard; cE
XX AAA51158;
XX AAA51158;
XX 26-SEP-2000 (first e
XX Plant-optimized mutan
XX Heat-labile toxin; CT
XX djuvant; anti-bacter
XX vibrio cholerae.
OS Synthetic.
YAA5
FT CDS /*TAG

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                                                                   CC This plant-codon optimized cDNA encodes a mutant synthetic Vibrio cholerae cholera toxin (CT) A submit (CT-A) having a 563K CC substitution. The sequence has no cryptic signal sequence and no CG (potential methylation sites) sequences. Novel polynucleotides encode a CC mutant Escherichia coli heat-labile toxin (LT) submnit A (LT-A) CC polypeptide or a mutant V. cholerae cholera toxin (CT) A submnit (CT-A) CC polypeptide, which have reduced enzyme activity as compared to the CC wild-type LT-A or CT-A polypeptide and where at least one of the codons C is altered to a plant preferred codon. The polynucleotide further CC comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible coronines, especially oral vaccines in transgenic plants for the prophylactic or therapeutic treatment against E. coli or V. cholerae. The coli mutant polypeptides are also useful as adjuvants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions elicit immune responses in animals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 snArgIleArgAspGluLeu
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ARNTZEN C J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fig 4B; 103pp; English.
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1..777
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/product= mutant_cholera_toxin_subunit_A
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alignment_scores:

Quality: 1084.00

Length:

240

211 A;

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seq_documentation_block:
ID         AAQ51332 standard;
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US-09-528-682-1 x AAA51158
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GGATTTGTGAGGCATGATGATGGATATGTGTCCACCAAGATTAGCTTGAG 25
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                                                                                                                                                                                                                                                      GluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLy 217
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                                                                                                                   snArgIleArgAspGluLeu 240
                                                                                                                                                                                          sValLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA 234
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                                                                                                    ATAGGATCAAGGATGAACTC
                                                                                                                                                                     GGTGAAGAGGCAAATCTTCTCAGGCTACCAATCTGACATTGACACCCACA
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                                                               /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAQ51332
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alignment_scores:
Quality: 1083.00
Ratio: 4.792
~~~~1arity: 94.167
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US-09-528-682-1 x AAQ51332
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                                                                                                                                                                                                                                                                                                                         The wild-type sequence coding for the A subunit of the cholera toxin (CT-A) (MeKalanos et al., Nature 306, 551 (1983) - see AAQ46318) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51327-Q51334). The invention relates to immunogenic, detoxified CT-A proteins and their use in vaccines to protect against Vibrio cholerae. Sequence AAQ51332 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation.
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P-PSDB;
 101
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misc_difference
                                                                                                                                                                                                                                                                                                   Sequence 723 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Fig 2 and Page 48; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-DEC-1991;
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protomer A; site-directed mutagenesis; reduced toxicity;
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                                                                                                   SATgSeTGlyGlyLeuMetProATgGlyHisAsnGluTyrPheAspATgG
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GCAGTCAGGTGGTCTTATGCCAAGAGGACAGAGTGAGTACTTTGACCGAG
               lyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThrGlnThr
GTACTCAAATGAATATCAACCTTTATGATCATGCAAGAGGAACTCAGACG
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DB; AAR44031.
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GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr

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seq_documentation_block:
ID AAQ51329 standard; DN
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AC AAQ51329;
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DT 08-DEC-1993 (first e
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DT 08-DEC-1993 (forst e
XX
Immunogenic detoxifie
KW protomer A; site-dire
KW protomer A; site-dire
KW protomer A; site-dire
KW ADP-ribosyltransferas
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FH Key Locat
FT misc_difference 289.
Yta
FT misc_difference 289.
Yta
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W09313202-A.
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PD 08-JUL-1993.
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                                                                                                                                                            Immunogenic detoxified CT-A; cholera vaccine; adenylate cyclase; protomer A; site-directed mutagenesis; reduced toxicity; ADP-ribosyltransferase activity; ss.
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                                                                                             Location/Qualifiers 289..291
                                                                   'note= "wild-type GTT(Val) mutated
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alignment_block:
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seq_documentation_block:
ID AAQ51333 standard; DN
AC AAQ51333;
AC AAQ51333;
AC AAQ51333;

DT 08-DEC-1993 (first e
XX Immunogenic detoxifie
KW Protomer A; site-dire
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   The wild-type sequence coding for the A subunit of the cholera toxin (CT-A) (Mekalanos et al., Nature 306, 551 (1983) - see AAQ46318) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51327-Q51334). The invention relates
                                                                                                                                                                                                               Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
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sValLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA
                                           GluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLy
                                                                                                                    LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl
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                              GAAAAAACCCAAAGTCTAGGTGTAAAATTCCTTGACGAATACCAATCTAA
                                                                                                                                                                            ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh
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                                                                           CGCCGGGTTGTGGGAATGCTCCAAGATCATCGATCAGTAATACTTGCGAT
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AGTTAAAAGACAAATATTTTCAGGCTATCAATCTGATATTGATACACATA

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seq_documentation_block:
ID AAQ51327 standard; DNA; 72
XX
AC AAQ51327;
XX
O8-DEC-1993 (first entry)
XX
Immunogenic detoxified CT-
KW Protomer A; site-directed
KW ADP-ribosyltransferase act
XX
Vibrio cholerae.
XX
KR (BOC-1991; Incation/OFT Misc_difference 156..158
FT // MO9313202-A.
XX
YO9313202-A.
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O8-JUL-1993.
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YO9313202-A.
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Domenighini M, Hol W, Pi
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US-09-528-682-1 x AAQ51327
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                                                                                                                   Align seg 1/1 to: AAQ51327
                                                                                                                                                                                                                                                                  Ratio:
Percent Similarity:
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/note= "wild-type GTT(Val) mutated to
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Seq.
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                                                                                                                                             _documentation_block: AAQ51331 standard;
                     Immunogenic detoxified CT-A; cholera vaccine; protomer A; site-directed mutagenesis; reduce ADP-ribosyltransferase activity; ss.
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451 AGTAACTTAGATATTGCTCCAGCAGCAGATGGTTATGGATTGGCAGGTTT
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                                                                                                                                                                                                            ATAGAATTAAGGATGAATTA
                                                                          Asn-107 cholera toxin subunit
                                                                                               (first entry)
                                                                                                                                                 DNA; 723
                                                                                                                                                                                                                                   240
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                                       reduced
                                                 adenylate cyclase;
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Vibrio cholerae

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic detoxified mutant cholera toxin and heat labile toxin - useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
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seq_documentation_block:
ID AAQ51330 standard; DNA; 72
XX
AC AAQ51330;
XX O8-DEC-1993 (first entry)
XX Encodes Ser-106 cholera to
XX Immunogenic detoxified CT-
KW Protomer A; site-directed
KW ADP-ribosyltransferase act
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The wild-type sequence coding for the A subunit of the cholera toxin (CT-A) (McKalanos et al., Nature 306, 551 (1983) - see AAQ46318) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51327-Q51334). The invention relates to immunogenic, detoxified CT-A proteins and their use in vaccines to protect against Vibrio cholerae. Sequence AAQ51330 is a combination of the wild-type coding sequence and the mutagenic
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seq_documentation_block:
ID AAA51160 standard;
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This plant-codon optimized cDNA encodes a mutant synthetic Vibrio cholerae cholera toxin (CT) A subunit (CT-A) having a R192G substitution. The sequence has no cryptic signal sequence and no CG (potential methylation sites) sequences. Novel polynucleotides encode a mutant Escherichia coli heat-labile toxin (LT) subunit A (LT-A) polypeptide or a mutant V. cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant-optimized mutant V. cholerae toxin A subunit G192
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                                                                                                                                                                                                                                      New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions.
                                                                                                                                                                                                                                                                                 WPI; 2000-442653/38.
P-PSDB; AAY96656.
                                                                                                                                                                                                                                                                                                                         Mason HS,
                                                                                                                                                                                                                                                                                                                                                  (MASO/) MASON H S.
(ARNT/) ARNTZEN C J.
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alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prophylactic or therapeutic treatment against {\tt E.} coli or {\tt V.} cholerae. The mutant polypeptides are also useful as adjuvants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 GCAATCAGGTGGTCTTATGCCAAGGGGACAATCTGAGTACTTTGACAGGG
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                                                                                 GluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLy
                                                                                                                                                                                                                                                      allleAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyr 150
                                                                                                                           roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn
                                                                                                                                                                                                ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh
                           GGTGAAGAGGCAAATCTTCTCAGGCTACCAATCTGACATTGACACCCACA
                                                                     GAAAAGACCCAATCTTTGGGTGTGAAGTTCCTTGATGAGTACCAATCTAA
                                                                                                              CACCAGGTTGTGGAAATGCTCCAGGUTCAAGCATGAGCAACACTTGTGAT
                                                                                                                                                      eProProAspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaP
                                                                                                                                                                                                                                          TGCTTGATGAGCAACTCCATAGGAATAGGGGCTACAGGGATAGGTACTAC
                                                                                                                                                                                                                                                                                    TGGAATCCCATACTCCCAAATCTATGGATGGTATAGGGTGCACTTTGGAG
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Ratio: 4.799
milarity: 93.333
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seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:AAQ31263
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                                                         SOUTHERN CALIFORNIA
                                                                                                                                                                                               /note= "Glull2 codon 588
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "first proposed authentic COOH
    recombinant end of Al"
                                                                                                                                                                           'note= "start of C-terminal truncation, see CC'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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alignment_block:
US-09-528-682-1 x AAQ31263
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                                                                                                                                                                                                                                                                                        117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant DNA encoding analogue of Vibrio cholerae catalytic sub-unit - useful as a vaccine for preventing cholera, has lit or no catalytic activity
                                                                                                                                                                                                                                                                                                                                                           101 LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl
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                    eProProAspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaP
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                                                                                                                                                       TGGGATTCCATACTCCCAAATATATGGATGGTATCGAGTTCATTTTGGGG
                                                                                                                                                                                                                                                                                                                                    TTAGGGGCATACAGTCCTCATCCAGATGAACAANNNGTTTCTGCTTTAGG
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seq_documentation_block:
ID ABA92644 standard; DN
XX ABA92644;
XX ABA92644;
XX ABA92644;
XX Cholera toxin; bacte;
XX 29-NOV-2001; 2000US-
XX 24-MAY-2000; 2000US-
XX (UYMA-) UNIV MARYLAN
XX POWell RJ, Hone D;
XX Introducing and expression and specific expression and specific codding the gene in animal cell comprise collipses containing a collipse collipse containing a collipse collips
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a gene in animal cells, comprising infecting animal cells with bacte blebs containing a eukaryotic expression cassette encoding the gene. The present invention also describes: (1) a bacterial bleb containing
                                                                        bacterial bleb containing a eukaryotic expression cassette including the polynucleotide coding sequence. The method can be used for introducing endogenous or foreign genes into animal cells using bacterial blebs as vectors. The method allows for the delivery of eukaryotic expression cassettes encoding the endogenous or foreign genes into animal cells or tissues, and is useful for expressing e.g. vaccine antigens, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Introducing and expressing a gene in animal cells, useful for delivering a therapeutic agent to the cells, comprises infecting animal cells with bacterial blebs containing a eukaryotic expression cassette encoding the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cholera toxin Al subunit sequence SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                         eukaryotic expression cassette; (2) a transformed animal cell including
a bacterial bleb, or a transfected product of the bacterial bleb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  755
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                                                                                                                                                                                                                                                                                             therapeutically treating an animal with a therapeutic agent encoded by a polynucleotide coding sequence, by transfecting the animal with a
                                                                                                                                                                                                                                                                                                                                                                     (3) a method of delivering a eukaryotic expression cassette to an
animal cell, comprising mucosal transfection; and (4) a method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method for introducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-2000; 2000US-206994P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Fig 3; 83pp; English
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                                                      immunoregulatory agents,
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in animal cells or tissues.

bacterial blebs

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seq_documentation_block:
ID     AAF74430 standard;
XX
AC     AAF74430;
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US-09-528-682-1 x ABA92644
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                                                                              seq_name:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: ABA92644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         containing the eukaryotic expression cassette can also be used to treat animal cells cultured in vitro. The method can be used in gene therapy. The present sequence represents the cholera toxin Al subunit sequence, which is used in an example from the present invention for the production of non-pyrogenic blebs containing a DNA vaccine.
                                                                                                             559
                                                                                                                                           186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7586 BP;
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                                                                                                                              lyCysGlyAsnSerSerArgThr 193
                                                                                                                                                                                                                                                                                                                                                                                                                                             yrValIleAlaThrAlaProAsnMetPheAsnValAsnAspValLeuGly 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTAGATATTGCTCCAGCAGCAGATGGTTATGGATTGGCAGGTTTCCCTCC
                                                                                                                                                                                                                                                  LeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProPr 169
                                                                                                                                                                                                                                                                                                                   eProTyrSerGlnILeTyrGlyTrpTyrArgValAsnPheGlyValIleA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCACTTAGTGGGTCAAACTATATTGTCTGGTCATTCTACTTATTATATAT 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspArgLeuTyrArgAlaAspSerArgProProAspGluIleLysArgSe
                                                                                                             GTTGTGGGAATGCTCCAAGATCA 581
                                                                                                                                                                        GGAGCATAGAGCTTGGAGGGAAGAGCCGTGGATTCATCATGCACCGCCGG
                                                                                                                                                                                                                                                                                                 TCCATACTCCCAAATATATGGATGGTATCGAGTTCATTTTGGGGTGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                            GCATACAGTCCTCATCCAGATGAACAAGAAGTTTCTGCTTTAGGTGGGAT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGTTATAGCCACTGCACCCAACATGTTTAACGTTAATGATGTATTAGGG
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                                                                            /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAF74430
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5.049
96.335
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Gaps:
Percent Identity:
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alignment_block:
                                                                                                                                                                                                                                                                                                       alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method for amplifying (A1) toxigenic CC vibrio cholerae nucleic acid by: (a) performing a polymerase chain CC reaction (PCR), by combining a medium containing toxigenic V. cholerae nucleic acid with an oligonucleotide primer (I) which will bind to a continuous containing toxigenic V. cholerae nucleic acid, in an environment suitable for CC carrying out PCR; (b) combining the medium with a second primer which CC will bind downstream to the first primer to a section of the CC complementary strand of the V. cholerae nucleic acid; and (c) amplifying CC complementary strand of the V. cholerae nucleic acid; and (c) amplifying CC corresponding sections of V.cholerae nucleic acid; and present in the medium. CC The method is useful for detecting toxigenic V. cholerae organisms or CC toxigenic V. cholerae nucleic acid, e.g., ctxA gene, in an environmental CC water sample e.g., tap water sample, river water sample, lake water CC sample or a sewage sample. The method is useful in PCR assays for CC detecting a microorganism or nucleic acid of the microorganism in a CC v. cholerae nucleic acid in a sample. The PCR method involving (I) is CC v. cholerae in water samples. The present sequence represents a creasent invention leaves of the v. cholerae ctxA gene, which is used in an example from the V. cholerae ctxA gene, which is used in an example from
                                                                                                                                                                                       Align seg 1/1
                                                                                                                                                                                                                       US-09-528-682-1 x AAF74430
                                                                                                                                                                                                                                                                         Percent Similarity:
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Vibrio cholerae nucleic acid for
organisms present in the sample
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                                                                                                                   GCCAAGAGGACAGAGTGAGTACTTTGACCGAGGTACTCAAATGAATATCA
                                                                   tProArgGlyHisAsnGluTyrPheAspArgGlyThrGlnMetAsnIleA 40
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seq_documentation_block:
ID AAF74431 standard; DNA; 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name:
                                 Novel oligonucleotide primer useful for PCR amplification of toxigenic Vibrio cholerae nucleic acid for detecting toxigenic Vibrio cholerae organisms present in the sample -
                                                                                                                                                                                                                    16-MAR-2000; 2000ZA-0001349
                                                                                                                                                                                                                                                                                                                              ZA200001349-A.
                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGCAGCAGATGGTTATGGATTGGCAGGTTTCCCTCCGGAGCATAGAGC
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                                                                                                           2001-191829/19
Fig
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 44pp; English
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seq_documentation_block:
ID AAT03448 standard; DN
XX
AC AAT03448;
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DT 02-MAY-1996 (first e
XX
DE Shigella flexneri the
XX

AAT03448 standard; DNA;

777

Shigella flexneri thermolabile enterotoxin

gene fragment LTf

(first entry)

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alignment_block:
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seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:AAT03448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC The present invention describes a method for amplifying (A1) toxigenic CC vibrio cholerae nucleic acid by: (a) performing a polymerase chain CC reaction (PCR), by combining a medium containing toxigenic V. cholerae CC nucleic acid with an oligonucleotide primer (I) which will bind to a section of V. cholerae nucleic acid, in an environment suitable for CC carrying out PCR; (b) combining the medium with a second primer which CC will bind downstream to the first primer to a section of the CC corresponding sections of the V. cholerae nucleic acid; and (c) amplifying CC corresponding sections of V. cholerae nucleic acid present in the medium. CC corresponding sections of V. cholerae nucleic acid present in the medium. CC corresponding sections of v. cholerae nucleic acid present in the medium. CC corresponding sections of v. cholerae nucleic acid v. cholerae organisms or CC corresponding sections of v. cholerae nucleic acid. e.g., ctxA gene, in an environmental cc water sample e.g., tap water sample, river water sample, lake water cample or a sewage sample. The method is useful in PCR assays for CC sample or a sewage sample. The method is useful for detecting toxigenic CC v. cholerae nucleic acid in a sample. The PCR method involving (I) is CC v. cholerae in water samples. The PCR method involving (I) is crapid, economical, specific and sensitive for detecting toxigenic CC v. cholerae in water samples. The present sequence represents a CC region from the V. cholerae ctxA gene, which is used in an example from the V. cholerae ctxA gene, which is used in an example from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AAF74431
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                                             CATCCAGATGAACAAGAAGTTTCTGCTTTAGGTGGGATTCCATAC
                                                                                                                            CTGCACCCAACATGTTTAACGTTAATGATGTATTAGGGGCATACAGTCCT
                                                                                                                                                hrAlaProAsnMetPheAsnValAsnAspValLeuGlyValTyrSerPro
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seq_documentation_block:
ID AAV62460 standard; DN
XX
AC AAV62460;
XX
DT 15-FEB-1999 (first e
XX
DE Helicobacter pylori u
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of the LTf fragment which encodes part of the thermolabile enterotoxin subunit. A sequence and all of the subunit. B sequence of Shigella flexneri. The DNA fragment is useful as a probe for specific detection of toxigenic enterobacteria.
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  Helicobacter pylori ureB-Vibrio cholerae A2+B subunit gene fusion
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alignment_block:
US-09-528-682-1
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                                                                                                                                                                 Ratio:
Percent Similarity:
                                                Align seg 1/1
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    137
                                                                                                                                                                                                                                                                                                                                                                         comprising the chimeric proteins for H. pylori-associated diseases such as gastritis, gastric ulcer, duodenal ulcer and gastric cancer (clained). The chimeric proteins are designed to have excellent immunogenicity, to be stable in the stomach, to penetrate the mucous membrane of the intestine, and to stimulate production of sIgA. They can additionally be used as active ingredients in diagnostic kits for H. pylori infection, and for production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 77-78; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New chimeric proteins for use against Helicobacter pylori comprising an antigenic protein of H. pylori and Al and B su of Vibrio cholerae toxin, preferably produced by recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-1997;
31-MAR-1997;
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1557 CAGAAATATCACTAAAAAAGACATGCAATTCAACGACACTACCGCTCACA 1606

229	213	196	179	163	152
1848	1798	17 4 8	1698	1648	1607
229 uValAspIleTyrAsnArgTleArgAspGluLeu 240 :::: ::: ::: 1848 TATTGATACACATAATAGAATTAAGGATGAATTA 1881	GluTyrGlnSerLysValLysArgGlnIlePheSerAspTyrGlnSerG1 229 	lyAspThrCysAsnGluGluThrGlnAsnLeuSerThrIleTyrLeuArg 2 ::::: ::: ::: ::: GTAATACTTGCGATGAAAAAACCCAAAGTCTAGGTGTAAAATTCCTTGAC 1	plleHisHisAlaProGlnGlyCysGlyAsnSerSerArgThrIleThrG 1	rgLeuAlaGlyPheProProAspHisGlnAla.TrpArgGluGluProTr 1::::::::::::::::::::::::::::::::::::	152AsnLeuAsnIleAlaProAlaGluAspGlyTyrA 1
	229	212	196	179	163
	1847	1797	1747	1697	1647

of: US-09-528-682-1 to: EST:*

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Search information block:
Query: US-09-528-682-1
Query length: 240
Database: EST:*
Database sequences: 13736207
Database length: -1841457050
Search time (sec): 4056.470000
  9b_est2:BG171693
9b_gsts:AZ698180
9b_est1:AA473437
9b_est2:BI910238
9b_est2:BI910238
9b_est2:BI910239
9b_est2:BG65351
9b_est2:BG859250
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9b_est2:BF364087
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Sequence
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b_gss:CNS04NYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -MODEL-frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spcol/US99528682/runat_18062002_082443_7797/app_query.fasta_1.689
-DB=EST -QEMT=fastap -SUFFIX=p2n.rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPEL-0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPOEXT=0.050 -XGAPOP=10.000 -XGAPOXT=0.500 -FGAPOP=6.000
-FGAPOEXT=7.000 -YGAPOP=10.000 -YGAPOXT=0.500 -DELOP=6.000
-FGAPOEXT=7.000 -YGAPOXT=1 -MAYRIX=510sum62 -TRANS=human40.cdi
-LIST=1000 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=50 -MODE=-LOCAL -OUTEMT=pfs -NORM=ext -HEAPSIZE=-500
-MINLEN=0 -MAXLEN=20000000000 -USER=US09528682_@CGN1_1_5309
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -MARN_TIMEOUT=30
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       y the GenCore software, version 4.5, Compugen Ltd.
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| BF65857 603301833F1 NIH_CGAP |
| BB618505 BB618505 RIKEN full-16 |
| AZ247543 RPCI-23-92P2.TJ RPCI-2 |
| BB619064 BB619064 RIKEN full-16 |
| AZ571452 287PvH02 Pv MBN #30 P1 |
| BG539191 60256883F1 NIH_MGC_77 |
| BF304330 601887226F1 NIH_MGC_1 |
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| BJ180858 BJ180858 normalized fu |
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1:AV935906
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gb_est2:BI332128
gb_gss:AZ394035
gb_est2:BI588980
gb_est2:BE347372
gb_est1:AA016910
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ORIGIN
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AUTHORS
TITLE
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gb_est1:AW765532
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LOCUS BF574917
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gb_est2:BM337299
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                                                    Align seg 1/1 to: BF574917
                                                                                                     US-09-528-682-1 x BF574917
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LeuTyrArgAlaAspSerArgPro...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: CLONETECH Laboratories, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999
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0.806
43.525
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/Clone=lib="NIH_MGC_81"
/clone_lib="NIH_MGC_81"
/lab_host="Diffusion of the property of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
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| AU148636 AU148636 NT2RM4 Homo s
| AW765532 daj73e05.yl Harland sta
| AA392265 LD11281.5prime LD Dros
| BM337299 MESST205-H03.T3 ISUM5-H
| BG641822 pg11c.pk002.d14 Chicke
| B132128 602981466F1 NCI_CGAP_I
| AZ394035 LM0157J20F Mouse 10kb
| B1588980 RH30611.5prime RH Dros
| B2347372 sp39b05.yl Gm-c1043 Gl
| AA016910 mh34f11.rl Soares mous
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334 AACTCTTTGACCCCATCATCTCGGATCGCCACGGGGGCTACAAACCCACT
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                                                                                             TTCTGTCGAAAAGGCGTGTCCCGTGTGCGGGCTCAGGATTGGCCGGATGG
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GCCAAGCCGGGTCTGGGCAAGGGACAGACTTCGG
                                                                                                                                        TyrLeuArgGluTyrGlnSerLysValLysArgGlnIlePheSerAspTy
                                                                                                                                                                                              CTAAACCTCTGAGAACATGAGGGGAAGAGCAGCAGAGTCATCGGATGACA
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CNS04NYY 812 bp DNA linea Tetraodon nigroviridis genome survey sequence T7 123D09 of library G from Tetraodon nigroviridis,

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                        63 rLeuSerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyT 80
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                                                                                 GCGCCCACATTCAGGTTGGTTAGATATGGAGCTCAGTATGTACAGCTAGA
                                                                                                                                                                      .....AGCGCCTGGCAGACGAGGCTGAGGGATCACAGTCAGGCA 173
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GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
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/db_xref="taxon:99883"
/clone="123D09"
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                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
Unpublished (1999)
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602322217F1 NIH_MGC_89 Homo sapiens
                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 939)
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EST.
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BG171693
                                                                                                High quality sequence stop:
                                                                                                                   Plate: LLAM10170 row: b column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             numan
                                                                                                                                                                           CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4425124"
                                                                            Location/Qualifiers
                                                                                                695.
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cDNA clone IMAGE:4425124
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGTCATGGCTGCTGAGAATATTCCTGAGAATCCCCTGAAGTATCTGTA 276
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/tissue_type="hypernephroma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 231 c 229 g 233 t
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Quality:
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 223 row: D column: 11 Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 714)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPCI-23-223D11.TJ RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Other_GSSs: RPCI-23-223D11.TV Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao,S., Nierman,W., Feldblyum,T., Malek,J.,,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ698180.1 GI:12415007
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                                                                                                             191
                                                                                                                             selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed in DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                             /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of ECORI and ECORI Methylase. Size
                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-223D11"
                                                                                                                                                                                                                                                                                   /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                            /sex="Female"
                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                             179 c
                                                                                                           181 g
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Mus musculus genomic clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shatsman, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           de Jong, P
                                                                                                                                           into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            end
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Percent Similarity:

Ratio:

90.50 1.708 66.250

Percent Identity:

Length: Gaps:

80 6 37.500

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SOURCE
ORGANISM
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US-09-528-682-1 x AZ698180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                       source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnMetAsnIleAsnLeuTyrAspHisAla...ArgGlyThrGlnThrGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vg77c10.rl Barstead MPLRB1 Mus musculus cDNA clone IMAGE.871986 5' similar to gb:x58295_rnal plasma GLUTATHIONE PEROXIDASE PRECURSOR (HUMAN); gb:U13705 Mus musculus domesticus C57BL/6J plasma glutathione (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 543)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                       Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 113.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project
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314 286 1810
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cl
                       /tissue_type="Kidney"
/dev_stage="6 weeks"
/lab_host="DH10B"
/note="Vector: pT7T3D
                                                                                                                                                           /strain="BALB/c"
/db_xref="taxon:10090"
/clone="IMAGE:871986"
                                                                                                                                      /clone_lib="Barstead MPLRB1"
                                                                                                                   /sex-"mixed"
                                                                                                                                                                                                                             organism="Mus musculus"
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  CDNA
                                                                 AUTHORS
TITLE
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SOURCE
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US-09-528-682-1 x AA473437
                                                                                                                                                                                                                                                               DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATACATTCCTTTTAAGCAGTATGCAGGCAAATATATCCTCCTTGTCAACG
                                              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1147)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies,
                                                                                                                                                                                                  EST
                                                                                                                                                                                                                                                               603069452F1 NIH_MGC_118 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                 BI910238.1 GI:16173620
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                                                   126 lyTrpTyrArgValAsnPheGlyValIleAspGluArgLeuHisArgAsn 142
                                                                                                                                                                         109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 rLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyTyrSerT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 spArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThr 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 ....LysArgSerGlyGlyLeuMetProArgGlyHisAsnGluTyrPheA 32
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                                                                                                                                                                                                                                                                                     PheAsnValAsnAspValLeuGlyValTyrSerProHis.....ProTy 109
                                                                                                                                                                                                                                                                                                                                                                                                     hrTyrTyrIleTyrValIleAlaThrAla......ProAsnMet 94
CTAGCGCACACCCCCGAAAGCCCCCGGCAGACACAAGGGCACATGGCTCG
                                                                                                                                                                      rGluGlnGluValSerAlaLeuGlyGlyIleProTyrSerGlnIleTyrG 126
                                                                                                                                                                                                                                  CAACACCAAC.....ACACCAACCCGGAAGCCACATCGCAGACCGTA
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Location/Qualifiers
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Plate: LLAM11548 row: h column: 13
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Clone distribution: MGC clone distribution info
found through the I.M.A.G.E. Consortium/LLNL at:
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/clone="IMAGE:5218236"
/clone=1b="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
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0.912
45.116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library." 422 c 294 g 104 t
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BASE COUNT
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LOCUS BI725716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 GlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCys 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isGlnAlaTrpArgGluGluPro.....TrpIleHisHisAlaPro 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            u.....AspGlyTyrArgLeuAlaGlyPheProProAspH 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est2:BI725716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvre,P., McDermott,J.P., Strager,J., Silflow,C. and Stern,D. Analyses of the Chlamydomonas reinhardthi Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1031080G02.yl C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Contact: Charles Hauser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
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EST.
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Durham, NC 27708-1000
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1 (bases 1 to 558)
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                           115
                                                                                            //note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: /note="Vector: pBluescript II library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (NH4+ - containing) and shifted to TAP - NO3- (24hrs); H2 production conditions (0, 12hr, 24hr) see Meils et al. (2000) Plant Phys. 122: 127-135; TAP + H202 (1, 12, 24 hr); TAP + sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). PolyA mRNA was purified from each sample, pooled and CONA synthesized. The cDNA was directionally cloned into lambda ZAP clones by superinfection with ExAssist (Stratagene) in the EcoRI (5') and XhORI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chauser@duke.edu
        (Stratagene) phage. The librar method 4 described in Bonaldo Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="C. reinhardtii CC-1690, Stress II (normalized
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                                                                         et al., (1996)
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alignment_scores:

Quality:

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SOURCE
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US-09-528-682-1 x BI725716/rev
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LOCUS AQ159897
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                                                                                                                                  source
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                                                                                                                                                                                                                                                           Clemson University
100 Jordan Hall, Cl
Tel: 864 656 5737
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone mgxb0002M14r, DNA AQ159897
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698 bp DNA linear GSS 09-SEP-1998 mgxb0002M14r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0002M14r, DNA sequence.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                                                                                                                                                                           Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M., Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                            Clemson University Genomics Institute
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                                                                                                                                                                                                                                                                                                                                                                     Contact: Dean RA
                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 698)
                                                                                                                                                                                                                   primer: GGAAACAGCTATGACCATG
                                                                                                                                                                      quality sequence stop: 417
                                                                                                                                                                                               BAC ends
                                                                                                                                                                                                                                       rdean@clemson.edu
                                                                                   /organism="Magnaporthe grisea"
/strain="70-15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.630
49.091
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/clone_lib="CUGI Rice Blast BAC Library"
                                                                                                                                                  Location/Qualifiers
                                                                   /db_xref="taxon:148305"
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US-09-528-682-1 x AQ159897/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 IleTyrGlyTrp 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 isProTyrGluGlnGluValSerAlaLeuGlyGlyIleProTyrSerGln 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 tPheAsnVal......AsnAspValLeuGlyValTyrSerProH 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 PheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC012102 1982 bp mRNA linear HT Homo sapiens, Similar to protein tyrosine phosphatase, receptor-type, F, clone IMAGE:4661274, mRNA.
Direct Submission
Submitted (02-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor-type,
BC012102
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                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           than 25X genome coverage. High density are available upon request."
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 yGlyLeuMetProArgGlyHisAsnGluTyrPheAspArgGlyThrGlnM 37
                                                                                                                                                                                                           sLeuAlaGlyGlnSerIleLeuSerGlyTyrSerThrTyrTyrIleTyrV 87
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TyrSerProHisProTyr:..
                                                                                                 alileAlaThrAlaProAsnMetPheAsnValAsnAspValLeuGlyVal 103
                                                                                                                                                                                                                                                               AGGGTTCCTCCAGGAAGGCTCCAGGAAGACCTGGCCAGAGGATAGGCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAAAGCACACTGTCCACTCGCTCCCAGCAAAGAACATCTGGAACACACC 1412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
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BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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NIH-MGC Project URL: ht
Contact: MGC help desk
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Tissue Procurement: ATCC
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/tissue_type="Colon, ader
/clone_lib="NIH_MGC_15"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
a 539 c 586 g 436
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38.750
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/db_xref="taxon:9606"
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LOCUS BI663851
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                                                                                                                                                                                                                                                                                                                             Contact: KODELL CONTROL REMAIL: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

Tissue Procurement: Jeffrey Green M.D.

Tissue Procurement: Jeffrey Green M.D.

Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                           High quality sequence stop: 
Location/Qualifiers
                                                                                                                                                                                                                  http://image.llnl.gov
Plate: LLAM11824 row: e column: 01
                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
1 (bases 1 to 1426)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technolo cDNA Library Arrayed by: The I.M.A.G.E.
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating
/dev_stage="5 months"
                                                                                                                                                               1. .1426
                                                                             /clone="IMAGE:5324904"
                                                                                                /db_xref="taxon:10090"
                                                                                                                    /strain="FVB/N"
                                                                                                                                       /organism="Mus musculus"
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                    ductal carcinoma"
                                                                                                                                                                                                                                                                                                                     Consortium (LLNL)
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alignment_block:
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TCCCGCTCGCTTTTCCATGCTAGTACAACGC
                                                                                                                                                   CGAGAGCCTGGGCTGAGATATAGTCGTTCTTACGCTCCAACATGGGAACG
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                                                                                                                                                                                                                                                                           TGCAGCGATGTTTCATTTCACGTTCGGACTCCATGGGCCTATGTTTGTGC 434
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                                                                                                      g...ValAsnPheGlyValIleAspGluArgLeuHisArgAsnArgGluT 145
                                                                                                                                                                                         .....GlyGlyIleProTyrSerGlnIleTyrGly.....TrpTyrAr 129
                                                                                                                                                                                                                                                                                                                                                                                                          GACCATAAACGATGCGCAAAATTCGAGTGTGATCATGGTACTCTAGGACT 484
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo of
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
a 379 c 404 g 333 t 1 others
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41.176
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Percent Identity:
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497 bp mRNA linear EST 11-FEB-1997 mr78g11.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:603620 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free tl
IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dul
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
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EST.
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h quality sequence stop: 415.
                158
/db_xref="taxon:10090"
/clone="IMAGE:603620"
                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="NIH/Swiss"
                                                                                                                                                                                                                /sex="pooled"
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                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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v) for further information.
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alignment_block:
US-09-528-682-1 x AA145382
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                      AUTHORS
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Grossman, A., Davies, J., Federspiel, N., Harris, E., Le McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R.
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                                  Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 686)
                                                                                             Chlamydomonas reinhardtii
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                                                                                                                   Chlamydomonas reinhardtii.
                                                                         Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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                                  aGluAspGlyTyrArgLeuAlaGlyPhePro......
                                                                                                                                                                                                               IlePro.....Tyr.SerGlnIleTyrGly...TrpTyrArgValA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAACTCTGGCCATCACATTCCCTCAGTGGGGCTAGGCGTGTACAAGTCGG
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                                                                                                                                                                                                                                                                                                                                                                                ACCCCTGGTGAGGAAACGTACGGCGCCGTACTGTCAGCGCTGCGGCTGGG
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                                                                                                                                .....ArgAspArgTyrTyrArgAsnLeuAsnIleAlaProAl 158
                                                                                                                                                                                                                                                                                  ATACCGCCACGTTGATACGGCACAGGTGTACGGCAATGAGGCCGATGTGG
                                                                                           AGCAAGCTGTGGCGAGACGCGTACGGCTATGACAGGGCCCCTGGCGGCTGT
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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Contact: Charles Hauser
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Unicellular System for Analyzing Gene Function and Regulation
Vascular Plants; project phase 2
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/Strain-"CC-1690 wild type mt+ 21gr"
/db_xref-"taxon:3055"
/clone_lib-"C. reinhardtii CC-1690, normalized, Lambda Zap
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                                                      266 AC...CTGTCCCACGCCAGGACGGCAGAGCCATGCTG.....CACTCG
                    46
                                                                                            29 luTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAla 45
                                                                                                                                                                 ArgGlyThrGlnThrGlyPheValArgTyrAspAspGlyTyrValSerTh
                                                                                                                                        CCGGAGGATGGACGCCGGTCTGGAGGAGATGTCCCTGCACGGCCACCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of scale clone-end sequencing project of the Tetraodon nigrovegenome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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183NO5 of library G from Tetraodon
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Human gene number estimate provided by genome wide analysis using
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2 (bases 1
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/note="Genoscope sequence ID : COAG183CG03LP1~end
340 c 274 g 127 t 1 others
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/db_xref="taxon:99883"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCGAGGAGCGGGCACCTGGGCACCAACTTCTACAACCCCTACGGGAA 617
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                                                                                                                                                                                                          Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shroshiyuki and Piero Carninci (RIKA) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 931)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
BI546037
                                                                                                                                       http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5259786"
/clone_lib="NIH_MGC_95"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 lnSer.....IleLeuSerGlyTyrSerThrTyrTyrIleTyrValIle 88
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                                                                                                                                                                                                                                                                                                                        uGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLysV 218
TTGAGCAGATGTGTATCACCCAGTACGAGAGGGAATCTCAGGCCTAT 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProProAspH 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .........GGCGGCTACGTGCTGGGAAGTGCCATGAGCAGGCCCATC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       erGlnIleTyrGlyTrpTyrArgValAsnPheGlyValIleAspGluArg 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTACAGC...AACCAGAACAACTTTGTGCAC......GACTGC 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGTTACCCCAACCAAGTGTACTACAGG.......CCCATGGATG 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGGGGGCAGCCCCATGGTGGTGGCTGGGGACAGCCTCATGGTGGTGGC 317
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/lab_host="DH10B"
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: segrefégenoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces marxianus var. marxianus, Pichia acquista, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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Pichia farinosa
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Saccharomycetales; Saccharomycetaceae; Pichia.
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/note="end : T7"
1 209 c 216 g
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1.149
53.623
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LOCUS AA979627
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Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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1 (bases 1 to 539)
                                                                                                                                                                                                                                                                                                        Email: http://www.fruitfly.org/EST, Plate: 343 row: C column: 3 High quality sequence stop: 446.
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                                              XhoI; Sized
                                                       /clone_lib="LD Drosophila melanogaster embryo pOT2"
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                                                                                                                                                                                                                                                                                   Location/Qualifiers
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/db_xref="taxon:7227"
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                    130
                    132
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               REFERENCE
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           Japanese medaka.
Oryzias lattpes
Cryzias; Netazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Neoteleostei;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryziinae; Oryzias.
1 (bases 1 to 765)
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                                                                                   433
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                                                                                                                                                                                                               185
                                                                                                                                                                                                                                                                                          169 ProAspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaProGl 185
                                                                                                                                                                                                                                                                                                                                  532 GGGTAAGGCAGGTTGTATTTCTGCAGGTTTGCATACAGGCCGGTTTC...
                                       214 TyrGlnSerLys 217
                                                                                                                                                                                                                                                                                                                                                                                  163 rgLeu....
                                                                                                                                                                                                                                                                                                                                                                                                                            582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 gAspArgTyrTyrArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            614 CTGTCCTGG......GTAGAGCTCCTTCGCCAAAGTAA 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 ValAsnPheGlyValIleAspGluArgLeuHisArgAsnArgGluTyrAr 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 lylleProTyrSerGlnIleTyr......GlyTrpTyrArg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    687 GAGTGTAGCAGCG..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 uGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGlyG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 734 ATCTTCTTTTCAAGACCTGCAACTCGCTCCAGAGTGTC...GATGTTCT
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                                                                                                                       luThrGlnAsnLeuSerThr......IleTyrLeuArgGlu 213
                                                                                                                                                                                                        nGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsnGluG
                                                                                                                                                                                                                                                                                                                                                                                                                            AGAACGGTTCTGGATGTTTCTTAAAGTAATCTATCTGGAAGATGGCTTCT
TTCCAGAGTCAG 372
                                                                                   ATGCAGATGATGTTTTACATTTGCCGCTCTTTATATACTGAGCCACTCC
                                                                                                                                                                   .....AATTCCAGCAGA.....TGTGGAGATTCCTGCACCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4.9-1, Inage, Chiba 263-8555, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: kmita@nirs.go.jp
method:uni-directional sequence direction:sequenced from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
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/sex="female/male mixed"
/tissue_type="brain"
/dev_stage="adult"
/dev_stage="adult"
179 c 189 g 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:8090"
/clone="br5314"
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1.077
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Gaps: 10
Percent Identity: 24.675
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REFERENCE
AUTHORS
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VERSION
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US-09-528-682-1 x AZ676739
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ORIGIN
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LOCUS AZ676739
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                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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                                                  302 TGTTACTGGACTATATACTTTAACTGTACATCCTTATAGCCCCTAATTTA.
                                                                                                                                        273 TACTATATTTAATAACAAGTACA...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
114 erAlaLeuGlyGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgVal
                                                                                        99 pValLeuGlyValTyr.....SerProHisProTyrGluGlnGluValS 114
                                                                                                                                                                                   83 TyrTyrIleTyrValIleAlaThrAlaProAsnMetPheAsnValAsnAs 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_gss:AZ676739
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Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Entamoeba histolytica.
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ676739 849 bp ENTIA77TR Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA library
Seq primer: M13-Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: bjloftus@tigr.org
Clones are derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Eukaryotic Genomics
The Institute for Genomic Research
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Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences
HMI: HMSS sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
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Location/Qualifiers
1. /849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_l: Bst I; Constructed at The
/note="Vector: pHOS1; Site_l: Bst I; Constructed at The
Institute for Genomic Research (FIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and Barell, Oxford University Press, 1999)."

120 c 116 g 293 t
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1.273
46.809
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/strain="HM1:IMSS"
/db_xref="taxon:5759"
                                                                                                                                                                                                                                     from:
                                                                                                                                                                                                                                                                                                                                                 Percent Identity:
                                                                                                                                          .....TCTAA
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JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATTTAAATATTCCTTCTGTAGTTGATGATAGAATAACAGAAGATTGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: rwing@clemson.edu
Total hq bases = 559
Seq primer: AATTAACCCTCACTAAAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Nov 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hordeum vulgare
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Location/Qualifiers
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864 656 4293
/clone="HV_CEA0009123f"
/clone="HV_CEA0009123f"
/clone=Llb="Hordeum vulgare seedling green leaf EST
library HVCDNA0004 (Blumeria challenged)"
/tissue_type="seedling green leaf"
/tissue_type="seedling green leaf EST
/tissue_type="seedling green leaf"
/tissue_type="se
                                                                                                                                                                                                                                                                                                                                                     /organism-"Hordeum vulgare"
/cultivar-"CI16155 (Mla13)"
/db_xref-"taxon:4513"
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alignment_block:
US-09-528-682-1 x BF264488
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                                                                                                                                                                                                                                                                                                                                                                                                                                            128 yrArgValAsnPheGlyValIleAspGluArgLeuHisArgAsnArgGlu 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 GCGATCCAAAATTAAACGAGCGTATTGGCCAGAATACTACTGTTACAGTT 138
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   = ro.....
                                                                                                      TTGTCGCCGTCGCCGTCGGCGTCCTGGCGCGCGCTTGGCGAAGCGGCC
                                                                                                                                                                                                                                                                                                  TyrArgAspArgTyrTyrArgAsnLeuAsnIleAlaProAlaGluAspGl 161
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                                                                                                                                                                  yTyrArgLeuAlaGlyPheProProAspHisGlnAlaTrpArgGluGluP 178
                                                                                                                                                                                                                                         CGAGCAAGTAGGATGTGGAAGACGGCACGGCATGCGCCTCCGCGTCCAGG
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TrpIleHisHisAlaProGln.....GlyCysGly
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REFERENCE
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                                                                                  GTGTTCTTTCCGATAAAAGTTACACATTGAAGACAACTCAGCAGCCATAT 55:
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                                                                                                                                                                                                                                                                             GlyLeuMetProArgGlyHisAsnGluTyrPheAspArgGlyThrGlnMe
                                    LeuSerLeuArgSerAlaHis.....
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TTGACGGAGAAGCTTGCTCATTTTCCTCAAAAGGTCTTCCATGCCTTGAA 501
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Seo,H.C., Kube,M., Edvardsen,R.B., Jensen,M.F., Beck,A., Spriet,E., Gorsky,G., Thompson,E., Lehrach,H., Reinhardt,R. and Chourrout,D. Miniature genome in the marine chordate Oikopleura dioica Science 294 (5551), 2506 (2001)
Contact: Seo HC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: hee-chan.seo@sars.uib.no
Insert Length: 1039 Std Error: 0.00
Seq primer: T7 and V4 (ATCCAACGCGTTGGGAGCTCT)
Class: shotgun.
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Fax: 55 58 4305
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Bergen High Technology Centre, Thormohlensgt. 55, N-5008 Bergen,
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Oikopleuridae; Oikopleura.
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199 c 223 g 326 t
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45.783
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/db_xref="taxon:34765"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Oikopleura dioica Shotgun Library"
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                                                                                  Clemson University
100 Jordan Hall, Clemson,
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaee; Oryza.
1 (bases 1 to 845)
Wing,R.A. and Dean,R.A.
8 BAC End Sequencing Framework to Sequence the Rice Genome
                                                                                                                                                                                        Unpublished (1998)
Contact: Wing RA
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                     Seq primer: GTAAAACGACGGCCAGTGClass: BAC ends
                                                                                                                                                                  Clemson University Genomics Institute
High quality sequence start: 63
                                                          Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa.
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTCTCCACGAACCGCGACAAAAATTAT.....GTAGAGGGCGCTG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TyrValSerThrSerLeuSerLeuArgSerAlaH1sLeuAlaGlyGlnSe
                                GluAspGlyTyrArgLeuAlaGlyPheProProAspHisGlnAlaTrp 174
                                                                                                                                                                                                   rGlyTrpTyrArgValAsnPheGlyVallleAspGluArgLeuHisArgA 142
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AGATGGTATTCGATACATTTTGCTGTTTTCGATCGATCTCACAGTAAAA 103
                                                                                                GGTGTAATCACCGGAATCGTCACAATCGAAGAATCANAATCGAG.....
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                                                                                                                                                snArgGluTyrArgAspArgTyrTyrArgAsnLeuAsnIleAlaProAla 158
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EccRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
. CGACTAATTCACTTTCCNAATGAATTCGCGCTNTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBACIndigo; Site_1: EcoRI; Site_2: EcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for genomic studies. In order to facilitate positional
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/tissue_type="Leaf"
/lab_host="E. coli DH10B"
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1.431
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seq_documentation_block: LOCUS BE972508
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74 GlnSerIleLeuSerGlyTyrSerThrTyrTyr.IleTyrValIleAlaT 90
                                                                                                       ACGCCTACGTGCAACTATCTATA.....
                                                                                                                                                                                           spGlyTyrValSerThrSerLeuSerLeuArgSerAlaH1sLeuAlaGly 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 1040)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon.9606"
/clone="IMMGE:3935368"
/clone="ID="IMH_MGC_82"
/clone="ID="IMH_MGC_82"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: testis; Vector: pbNR-LIB (Clontech); Site_1:
/note="Organ: pbNR-LIB (Clontech); Site_1:
/note="Organ: testis; Vector: pbNR-LIB (Clontech); Site_1:
/note="Organ: tes
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329 /
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46.448
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Gaps: 9
Percent Identity: 24.590
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LOCUS AG031102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_gss:AG031102
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              621 TATGTCCCTATCTATTACAACAAACACTGGAAACTGGACCTCGCTCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 HisProTyrGluGlnGluValSerAlaLeuGlyGlyIleProTyrSerGl 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        snSerSerArgThrIleThrGlyAspThrCysAsnGluGluThrGln 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProProAspHisGl 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAACACCCACGAGGCACATGGACGGACACACACACAGGAGGCAACGTC 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCAGGCAATCAGCACAATCCAAACACCCACATCATACAAGGCCGAACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hrAlaProAsnMetPheAsnValAsnAspValLeuGlyValTyrSerPro 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nAlaTrpArgGluGluProTrpIleHisHisAlaProGlnGlyCysGlyA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCCCAACAGACAGGGCAACACGGACAGCACCCAAGCCAAGCGACCACAG 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isArgAsnArgGluTyrArgAspArg...TyrTyrArgAsnLeuAsnIle 155
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-Chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC ences generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AG031102.1 GI:16557975
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan troglodytes DNA, clone: PTB-003L01.R, AG031102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y
                                                                                                                                                                                                                                                                                                                                                                                                            clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inpublished
                                                                                                                                                                                                                                                                                                          LIBRARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .AGCAACACCCCGCGCGGAAACCCCAGCGACACAACAGACACAA 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 1068)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (sites
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                                                                                                                                                                                                                                                                        Vector
                                                                                                                                                                                                                                                                                                                              Sequencing: M13Rev
                                                                                                                                                                                                                                                                                                                                                                                                     tracking errors.
                                                                                                                                                                                                    ector : pKS145
.Site 1 : SacI
.Site 2 : SacI.
                                                                   /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                       1. .1068
                                                                                                                                                                  Location/Qualifiers
          /sex="male"
                                     clone="PTB-003L01.R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..CCACCACAA......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Taylor, T.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_lib:PTB Chimpanzee Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear GSS 01-NOV-200 genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yada,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS 01-NOV-2001
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ORIGIN
                                                                                                     COMMENT
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LOCUS BF429191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est2:BF429191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: AG031102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                    TITLE
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                                                                                                                                    JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 alIleAlaThr......AlaProAsnMetPheAsnValAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 TyrValSerThrSerLeuSerLeuArgSerAlaHisLeuAlaGlyGlnSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 rIleLeuSerGlyTyrSerThr.....TyrTyrIleTyrV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGGTGCCCGTCATAANGGGAAAGGGGGGTGGGAAGGCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aGlyPheProPro...AspHisGlnAlaTrpArgGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACACCCGCACGATGAGA.....CGTGCAAATGTAGGTGTCGAGAGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aLeuGlyGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspValLeuGlyValTyrSerProHisProTyrGluGlnGluValSerAl 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCTACCTACTCAATATCATTGTCCGATTCCGCGTGGTTTCTCATTGACA
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Triticae; Triticum.

(bases 1 to 370)

Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han Anderson,O.D., Chao,S., Lazo,G.R., Malatrasi,M., Miller,R., P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Malatrasi,M., Miller,R., P.S., Hsia,C.C., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D. Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D. The structure and function of the expressed portion of the when the structure and function of the converse of the structure and function of the structure and structu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF429191 370 bp mRNA linear EST: WHE1709_E10_I19ZS Wheat heat stressed spike cDNA library aestiyum cDNA clone WHE1709_E10_I19, mRNA sequence.
                                                            Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
                                                                                                                                                                                                                                                                                                                                                                Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
; Triticeae; Triticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF429191.1
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      Buchanan Street,
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Area, Western Regional Research Center
Buchanan Street, Albany, CA 94710, USA
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/clone_lib="PTB Chimpanzee Male BAC Library"
1 426 c 171 g 176 t 125 others
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EST 29-NOV-2000

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Zhang,D. of the wheat

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629 98 87 729 75

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alignment_block:
US-09-528-682-1 x BF429191
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                                                                             seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 CCCAAGTAGAGGAGAAGCTTGGGGCCCGTCCCCCATGGCTTGTCCACCGAC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 eProProAspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
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                                                                                                                                                                                                                                                                                                                                                                                GAACTCGGCCGAGAAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                            nGluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCGAGGTTGTCCAGAGGGAGTCCGAGTCGATCTCGAGGAAGACCCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAAGCTCCAAGTCAATGCCGAGGAGGAGCAGCGACGACGTGGGCGACTTT
                                                                                                                                                                                                                            AspIleTyrAsnArg 235
                                                                                                                                                                                GACATCTTCCTGAGG 336
                                                                                                                                                                                                                                                                             AGGTCTCCAGGCTCATGGACATCATCATCACTCACTCTACAGCAACAAG
                                                                                                                            gb_est2:BF422183
BF422183 614 bp FM1_12_G12.b1_A003 Floral-Induced propinguum cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 5105595818
Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5105595773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Spikes at 5, 10, 15 and 20
days after anthesis were heat stressed under two
conditions at Texas Tech University (D. Zhang in HT Nguyrn
lab): (1) at 38 C for 4 hours and (2) 5 days of cyclic
treatment of 38 C for 4 hours. Total RNA and poly(A) RNA
were prepared, a cDNA library was made, and the cDNA
clones were in vivo excised to give pBluescript phagemids
in the TJ Close lab (Choi, Close, Fenton, Malatrasi) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

80 a 114 C 104 9 71 t 1 others
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60.674
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_
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/tissue_type-"Whole spike"
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1 (FM1) Sorghum
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REFERENCE
AUTHORS
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US-09-528-682-1 x BF422183
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182 HisAlaProGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspTh 198
                                                                                                                                                                      278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                 178 TGGTACCGACAGCAGTAACGTAGCTCACTTCCGCCACTTTGACAAGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                            127 TrpTyr.....ArgValAsnPheGlyValIleAspGluArgLe
                                                                                                                                                                                                                 yrArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeu.AlaGl 166
                                                                                                                       yPhePro...ProAspHisGln.AlaTrpArgGluGluProTrpIleHis
                                                                                                                                                                      GAGCGCCTCTACGAGGAGCGCCAGAAGAGGAAGGCCACAGAGTCCTCGGG
                                                                                                                                                                                                                                                                     CCATCGACAGGTATGTCGGGAGGGTCGCAGGACGCGACGAGGGCGAGGTC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF422183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: JEN REV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mmpratt@uga.edu
Sequences have been tr:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Botany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An EST database from Sorghum:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Floral-Induced Meristem 1 (FM1)"
/note="Organ: Floral-Induced meristems; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
ECORI; mature plants were placed in a growth chamber for
15 days with 16 hr darkness and 8 hr light (flowering is
induced by short-day conditions); 16 days after being
returned to the greenhouse under natural long days during
late April/early May, meristems were harvested The
library was made from poly-A RNA in the cloning vector
lambda ZAP II. Clones to be sequenced were prepared by
mass excision."
95 a 148 c 177 g 94 t
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1.352
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alignment_block:
US-09-528-682-1 x BI658957/rev
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LOCUS BI658957
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                                                                                        Align seg 1/1 to reverse of: BI658957
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                                       SerGlyGlyLeuMetProArgGlyHis.....
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Ratio:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: Lothar Hennighausen Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
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                                                                                                                                                                                                                                                                                                                                                           Library."
a 174 c
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally, Primer: Oligo dT. Sverage insert 2.5 kb. Library constructed by Life Technologies, catalog # 12018-016. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH
                                                                                                                                                                                                    82.50
1.086
43.931
                                                                                                                                                                                                                                                                                                                                                                                                     Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996). Note: this is a NCI_CGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="NIH_CGAP_Mam4"
/tissue_type="tumor, gross tissue"
/lab_host="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:5347497"
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LOCUS BB618505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 CATTCTATAGCTTTATACTTCTACATCTCCACAC......CACC
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                                                                                                                                                                                                                                              Arakawa, T., Carninći, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB618505 RIKEN full-length enriched, 8 ccDNA clone 5730407E15 5', mRNA sequence.
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N.,
                                                                                                                                         Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(SSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                    Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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           Shibata, K.,
                                                                                                                                               230-0045, Japan
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ACTAGCTCACTTCATCTCCAGCTCCCAGCTAAGTGGGACTCAGCTTCTGA 205
                                              ......IleProTyrSerGlnIleTyrGlyTrpTyrArgValA 131
                                                                                                           CCACACCCACACCGCACTCGCCCAGAGACAAACTTAAGGTCAGGACGAGC
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Ratio;
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Yamanaka, I. Kiyosawa, H., Kondo, S., Salto, T., Shinagawa, A., Alzawa
KK., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T.,
Ishil, Y. and Hayashizaki, Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Func. Genomics 2 pre, L72-L86 (2001)
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
%atahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Kayat I Okeaki, M., Waraki, M., Waraki, M., Matsuura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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175 c 127 g 126 t
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53.247
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/lab_host="DH10B"
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/clone="5730407E15"
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/strain="C57BL/6J"
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                                                                                                                                                 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 92 row: P column: 2
                                                                                                                                                                                                                                                                                                                                                               Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                           Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Other_GSSs: RPCI-23-92P2.TV
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                                                                                                                                                                                                                                                                                                         Email: szhao@tigr.org
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 eGlyValIleAspGluArgLeuHisArgAsnArgGluTyrArgAspArgT 149
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                                                                                                                                                                                                                                                                             .HisHisAlaProGln..........GlyCysGlyAsnSerSerArgT
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                                                                                                                                .CTGTGTCAAGTTGACACCCAAAAC 34
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
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Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
hayashirayi y
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
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Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.

Func. Genomics 2 pre, L72-L86 (2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. : 11 (2), 281-289 (2001) Yamanaka, I., Kiyosawa, H., Kondo, S., Salto, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing pipeline with 384 multicapillary sequencer. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN Mouse ESTs (Arakawa, T., et al. 2001) Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB619064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               further details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN integrated sequence analysis (RISA) system -- 384 - format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-based methods for the mouse full-length cDNA
                                                                prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory
prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length
                                                                                                                                                                RIKEN. Division of Experimental Animal Research
                                                                                                                                                                                                                                                                                                           /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                            /dev_stage="8 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RIKEN full-length enriched, 8 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="5730471122"
                                                                                                                                                                                                                                                                                                                                                                                                               /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 634
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                                                                                                                                                                       oratory in
in Riken
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BASE COUNT
ORIGIN
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                                                                                                                                            seq_documentation_block:
LOCUS AZ571452
 REFERENCE
                                                                                                                                                                                                seq_name:
                                                                     KEYWORDS
                                                                                                                             DEFINITION
                                                                                         VERSION
                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197
                                                                                                                                                                                                                                                                                                                                                                             376 TGCCATGCAAATTTTATCGAGACCCTACAGCATTTGGCTCAGGAATCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                  198
                                                                                                                                                                                                                                                                                                       426 AAAATCCGCATCAAGTGGACCAAGCTAACTTCAGATTACCTCAGGGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 uAlaGlyPheProProAsp......HisGlnAlaTrpArgGluG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 ProHisProTyr.....GluGlnGluValSerAlaLeuGlyGly..... 118
                                                                                                                                                                                                                                                                    230 lAspIleTyr 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 CCACACCCACACCGCACTCGCCCAGAGACAAACTTAAGGTCAGGACGAGC 102
                                                                                                                                                                                                                                    AGATGTCTTC 485
                                                                                                                                                                                                                                                                                                                                         lnSer.LysValLys...ArgGlnIlePheSerAspTyrGlnSerGluVa 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         luProTrpIleHisHisAla.....ProGlnGlyCysGlyAsn 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTAGCTCACTTCATCTCCAGCTCCCAGCTAAGTGGGACTCAGCTTCTGA 152
                                                                                                                                                                                                                                                                                                                                                                                                            rCysAsnGluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ... AGCAGAACAAGCCAAGGTCTTCTCTCACCGAGGTGGCAACGTGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerSerArgThrIleThrGly.....AspTh 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAGTTATTCACATCCAAGCAGAAAATGGCCCCCGTCTACTTGTGGA...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTGGGCTGACCACCTTTCAGACAGCTACACTCCTCCAGATCAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgTyrTyrArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLe 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTGGAAT.....TCAGGACAAGCAGAGAAGAGTCTGAGCTACAAGGAT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           snPheGlyValIleAspGluArgLeuHisArgAsnArgGluTyrArgAsp 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_gss:A2571452
                                 malaria parasite P. vivax.
Plasmodium vivax
                                                                                                          287PvH02 Pv MBN #30 Plasmodium AZ571452
                                                                                      AZ571452.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
1 (bases 1 to 687)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB619064
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1.000
53.247
                                                                                         GI:13983551
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Gaps:
                                                                                                                     vivax genomic
                                                                                                                                          DNA
                                                                                                                                        linear
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                                                                                                                     DNA sequence
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COMMENT
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US-09-528-682-1 x AZ571452
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TITLE
JOURNAL
                                                                                                             151
                                                                                                                                                                                                                    107
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201 GAGACAACATCGTTTCGCGCGCCTGGACGCAGAAGCTCTGCTTGTTGGGG
                                                        67
                                                                                                                                                          46 rgGlyThr......GlnThrGlyPheValArgTyr 55
                                                                                                                                                                                                                                                                                                                            66 AACATTCAAACGGGGCGCC.....ATTCAAACGAGGCGCCATTCAA 106
                                                                                                                                                                                                                                                                                                                                                                      29 uTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                    16 IleLysArgSerGlyGlyLeuMetProArgGly...........HisAsnGl ::::|||||||||||||::: ||||||||||||
                                                                                                             CCAAACGAACCGCCATCCAAACGAACCGCCGCGTCAAGCGCCGCTCTGGG
                                                                                                                                                                                                                  ACGGGGCGTCATTCAAATGGGGCGCCCCCCAAACGAAC.....CGCTAT
                                                  .....ArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyT 80
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Dept. of Pathobiology, College of Veterinary
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville,
Tel: 352 392 4700
Fax: 352 392 9704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carlton, J.M.-R. and Dame, J.B. The Plasmodium vivax and P. berghei gene sequence tag projects Parasitol. Today 16 (10), 409 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="vector: pBluescript SK(+) vector DNA, phagemid /note="vector: pBluescript SK(+) vector DNA, phagemid exclsed from lambda 2AP; Site_1: EcoR V; Site_2: EcoR V; Site_beat from P. vivax infected blood using the following methods: first, infected blood was activated by the addition of 0.5 ml of ADP (40mg/ml) per 10 ml blood. Then blood was passed over a column of acid washed 0.1 mm glass beads, then through a Plasmodipur filter, followed by passage through a column of pre-wet Whatman CF11 powder (1:2 ratio volume of blood to CF11), and finally centrifuged through a 50% percoll density cushion. Purified DNA was digested with mung bean nuclease in the presence of 44% formanide at 50cC as described (Vernick, K.D., Imberski, R.B., and McCutchan, T.F. 1988. Nucleic Acids Research 16:6883-6896). Digested DNA was blood for the presence of 44% formanide at 50cC as described (Vernick, K.D., Imberski, R.B., and McCutchan, T.F. 1988.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ571452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              over a Sepharose CL-2B column. Fractions in the size range 500bp-4kb were ligated into the Eco RV site of pBluescript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.00
0.837
47.573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Pv MBN #30"
/dev_stage="asexual blood forms"
/lab_host="Saimiri boliviensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="Salvador I (Collins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'db_xref-"taxon:5855'
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13
24.757
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_est2:BG539191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 GTGTGCAGCTGTATCTCAAGCGAATCGCAGCTTTTGCCCCTTCTTATTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGl 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCAACGTTTAAGTGAACCGACTTGAAGGTCCCGTTTTGCACGACGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTCCCTCCCGACTAC 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yrArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeu.AlaGl 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yValIleAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTTTGGGTACGGCTGCCCGTTGTTCATGAAAAGGCTCATCCCAGTGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValAsn.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        602566883F1 NIH_MGC_77 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                           Plate: LLCM1510
                                                                                                                                                                                                                                                                                                          http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human
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                                                                                                                                                                                                                                                                    quality sequence stop: 495.
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccqcctcggcc); Site_2: SfiI (ggccatctatggcc); S and 3 adaptors were used in cloning as follows: 5 adaptor sequence: 5 - CACGGCCATTATGGCC-3 and 3 adaptor sequence: 5 - ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3 (where B = A,
                                                                                                          /clone="IMAGE:4691349"
/clone_1ib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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seq_name: gb_est2:BF304330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGGGCATGCGGCGCAAACCCGGCTGACCCGGAGGAGGACGTGAGCAAAG
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1935)
                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                               Unpublished (1999)
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cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM1002 row: d column: 08
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a 240 c 223 g 157 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACCACAACACGTAGACAGACAACGGGTTCACAAAACCNCCCGATGGAAA 1476
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                                                                                                                                                                                                                                                                                                                                                            JI-M-BH1-ant-c-02-0-UI.T1 NIH BMAP_M_S2 Mus musculus UI-M-BH1-ant-c-02-0-UI 5', mRNA sequence.
                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 368)
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   Genome
                               discovery
                                                                                                Bonaldo, M.F.,
                                                                                                                                                                                                                               Mus musculus
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                                                          Normalization and subtraction: two approaches to
                                                                                                                                                                                                                                                                     house mouse.
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Res. 6 (9), 791-806 (1996)
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/lab_host="DH108 (phage-resistant)"
/note="Organ: muscle; Vector: porB7; Site_1: EcoRI;
/note="Organ: muscle; Vector: porB7; Site_1: porB7; 
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/clone_lib="NIH_MGC_17"
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                                                                                                Lennon, G. and Soares, M.B.
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                                                                                                                                                       Craniata; Vertebrata;
Sciurognathi; Muridae;
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                                                                                                                                                              Muridae;
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                                                              facilitate gene
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                                                                                                                                                           Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 rAlaLeuGlyGlyIleProTyrSerGlnIleTyrGly...TrpTyr...A 129
                                               166 lyPheProProAspHisGlnAlaTrpArgGluGluProTrpIleHisHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 LeuGlyValTyrSerProHisProTyrGlu......GlnGluValSe
                                                                                                                                                                                                                                                                                                                                                                                                                              60 CAGTCTGAATGGTTACCCCTACATGTTCCATCATGGAGACTGGTTCTGTG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 CTCTGTGTGTTCTCCAAACACCCCAATCCAGGAAATCTTCCAGCATGTCTA 59
                                                                                                                                                      rTyrArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaG 166
                                                                                                                                                                                                                                                                                                                       GGAAGTCTGTGGGGCTGCTGGTTCTCCGTCTAAGTGGACTGGTGCTCAAT 159
                                                                                                                                                                                                                GCCTACGTGACTCATCTACATGCTGAGTACAGCCGACAGAAGGACATCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
20892-9643, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: M13 Reverse
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                                                                                                                                                                                                                                              ....HisArgAsnArgGluTyr......ArgAspArgTy 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NHH.BMAP_M.SI library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NII_BMAP_M_S2 library is a subtracted library derived from NIH_BMAP_M_S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="UI-M-BH1-ant-c-02-0-UI"
/clone_11b="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
/lab_host="DH10B_(Life_Technologies)"
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1.273
48.485
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                                                                 Align seg 1/1 to reverse of: BJ180858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                      85 IleTyrValIleAlaThrAlaProAsn....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: tshini@genes.nig.ac.jp
A backbone of the vector is pBluescript II, that was in vivo
excised from a modified IPs phage vector (Mo bi Tec, Germany). XhoI
digested-5' end of cDNA is ligated to SalI site of the vector, and
the BamHI digested-3' end including poly-A tail is ligated to BamHI
site of the vector. cDNA instert could be amplified with
conventional T7 and T3 primers. This normarized full- length cDNA
library was generated basically according to the method described
in Genome Research 10, 1617-1630 (2000), Carninci, P. et al.
Protonemata were blended by the POLYTRON, and then cultivated on
the BCD medium containing 0.5um BA (benzylaminopurine) for 8 to 13
days under the continuous light.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 489 bp mRNA linear EST 24-JAN-200 BJ180858 normalized full length cDNA library, chloronemata, caulonemata and malformed buds Physcomitrella patens subsp. patens cDNA clone pphb29a23 5', mRNA sequence.
                                                                                                                                                                                                                    Quality:
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
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Carninci,P., Hayashizaki,Y.,
                                                                                                                                                                                                Ratio:
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                                                                                                                                                                                                                                                                                                                                                /organism="Physcomitrella patens subsp. patens"
/db_xref="taxon:145481"
/clone="pbh29a2"
/clone_lib="normalized full length cDNA library,
chloronemata, caulonemata and malformed buds"
/tissue_type="mixture of chloronemata, caulonema
malformed buds"
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lAsnAspValLeuGlyValTyrSerProHisProTyrGluGlnGluValS 114
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                                                                                                                                                                                                                                                                                                                                                                                                   A backbone of the vector is pBluescript II, that was in vivo excised from a modified IPS phage vector (Mo bi Tec, Germany). XhoI digested-5' end of cDNA is ligated to SalI site of the vector, and the BamHI digested-3' end including poly A tail is ligated to BamHI site of the vector. cDNA instert could be amplified with conventional T7 and T3 primers. This normarized full-length cDNA library was generated basically according to the method described in Genome Research 10, 1617-1630 (2000), Carninci, P. et al. Protonemata were blended by the POLYTRON, and then cultivated on the BCD medium containing 0.5mM BA (benzylaminopurine) for 8 to 13 days under the continuous light.
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Fujita,T., Shin-i,T., Seki,M., Kamiya,A., Uchiyama,T., Nishiyama,T.,
Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Physcomitrella patens subsp. patens.
Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center For Genetic Resource In
National Institute of Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tshini@genes.nig.ac.jp
                                                                                                                      /organism="Physcomitrella patens subsp. patens"
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chloronemata, caulonemata and malformed buds"
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                    tissue_type="mixture of chloronemata, caulonemata and
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169 g
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Length: Gaps:

Percent Similarity:

65.714

Percent Identity: 34.286

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VERSION
KEYWORDS
SOURCE
ORGANISM
BASE COUNT
ORIGIN
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US-09-528-682-1 x BJ187033/rev
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAGGGAT 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGTCCATCTCAGTGGGAAATGAACCTCTTTCCGAG.....TTTTAT 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 730)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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EST.
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BG250385
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                                                                                                                                                                                                                                                                                                                                                                                             http://image.llnl.gov
Plate: LLAM10289 row: e column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Consortium (Clone distribution: MGC clone distribution information can
                         184
                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 680.
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/clone_lib="NIH_MGC_90"
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/tissue_type="denocarionma, cell line"
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Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
197 c 181 g 168 t
                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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alignment_scores:

807

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mRNA

linear

EST 10-JUL-2001

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seq_documentation_block:
LOCUS BI199325
                                                          seq_name: gb_est2:BI199325
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US-09-528-682-1 x BG250385
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                                                                                                                                                                                                                                                                                                                                                                                                     .....AsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGly 166
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REFERENCE
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                       ATCCTCACCACCCCAGCCCCAGTATTCATTGGGGAAGCCATTCATC....
                               .....GlyIleProTyrSerGlnI 124
                                                                                       GGGCCGAGAGATCTTCATCCCAGCCAGGCGACCTGGTAGCAATGTCGTC
                                                                                                                                    GlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGly.. 117
                                                                                                                                                                                  CTTATCTCCTCGGTGCTTCACCATCT...TATAGTGTCCTACAGATGTGG 347
                                                                                                                                                                                                                                leTyrValIleAlaThrAlaProAsnMetPheAsnValAsnAspValLeu 101
                                                                                                                                                                                                                                                                              .TCTGGGTACGGACCAGGAGGTCAAATCTGTGGGGATTTTCCTCATTGCC 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 807)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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High quality sequence stop: 798.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="organ: brain; Vector: pOTB7; Site_1: xho1; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(6). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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1.095
48.052
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/clone_lib="NIH_MGC_19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
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BASE COUNT
ORIGIN
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AUTHORS
TITLE
alignment_block:
US-09-528-682-1 x BI152296
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                                                                                                                              alignment_scores:
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                                                               Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 GGCAACATGCGGGGTCCCCGGGGGTCACACACATACAGATTGTGGTCATT 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 ArgAsnArgGluTyrArgAspArgTyrTyrArgAsnLeuAsnIleAlaPr 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                                                          Quality:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1401)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 153.
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                                                                                      Ratio:
                                                                                                                                                                                                                       466
                                                                                                                                                                                                                providing samples: Gilbert Smith, NIH" 568 c 246 g 121 t
                                                                                                                                                                                                                                                             /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo Library constructed by Life Technologies. Investigator
                                                                                                                                                                                                                                                                                                                                               /tissue_type="spontaneous tumor, metastatic
Stem cell origin."
                                                             81.00
0.818
47.596
                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="CZECH II (feral)"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:5068039"
                                                                                                                                                                                                                                                                                                                          /lab_host="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                            clone_lib="NCI_CGAP_Lu29"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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                                                                 Identity:
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LOCUS BF345560
    COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CACGCAGCACCCTAC.....GGCACAAGCCCAAGAGCTAACTCATCCCC 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTAACTTCAAGAGCAAGAATGGGCACACACGGAAGAAGACTCACATCAA 85
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                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1576)
                                                                                                                                                                                                                5', mRNA sequence.
BF345560
                                                                                                                                                                                                                                            1576 bp 602019145F1 NCI_CGAP_Brn67 Homo
                                                                                                                                                                              EST.
                                                                                                                                                                                              BF345560.1 GI:11293155
Contact: Robert Strausberg, Ph.D
                                                                                                                                     Homo sapiens
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6
                                                                                         Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                    mRNA linear EST 22-NOV-2 sapiens cDNA clone IMAGE:4154602
                                    Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390
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                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                       EST 22-NOV-2000
                                                                                               Homo
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alignment_block:
US-09-528-682-1 x BF345560
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    196
                                                                                            179
                                                                                                                                               428
                                                                                                                                                                                   163 ArgLeuAlaGlyPheProProAspHisGlnAlaTrpArgGluGluProTr 179
                                                                                                                                                                                                                                      379
                                                                                                                                                                                                                                                                                    146
                                                                                                                                                                                                                                                                                                                                                                                                                     288 GAAGACCCTTACTACATGACACAAGGG.....ATCAGCATGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
                                                                                                                                                                                                                                                                                                                                329 TACAGATACACAGAAGAACTAGATAGAAGAGCGTACAACAAAAAGTACG
                                                                                                                                                                                                                                                                                                                                                                         134 lIleAsp......GluArgLeuHisArgAsnArgGluTyrA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 AGACCCCATTTGCGTGATGCAAGTAACGGTGATGACCATGCATTCCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 GGAATCGTATCGTATGTCCTGCATATCCTAGAACGGCATCCACTCTTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 GlyTyrSerThrTyrTyrIleTyrValIleAlaThrAlaPro.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGGCACATGAGGATTATATCCATATAAGAATTCAACAGAGAAACGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGly
                                                                                         pIleHisHisAlaProGlnGlyCysGlyAsnSerSerArgThrIleThrG
                                                                                                                                                                                                                                      CCTG. CAATGGCACAGAAATAGAACATCCGGAACTATGGAGACGTACTAC
                                                                                                                                                                                                                                                                                  rgAspArgTyrTyrArgAsnLeuAsnIleAlaProAlaGluAspGlyTyr
lyAspThrCysAsnGluGluThrGlnAsnLeuSerThrIleTyrLeuArg
                                                                                                                                          AGACTACAGGGTGACCCACCG.........
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Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence start: 3 High quality sequence stop: 299.
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                                              .CACCGACCATATGCC.....AGCGCCACGACGACCAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT Average insert size 2.3 &b. Constructed by Life Technologies. Note: this is a NCI_CGAP Library." 472 c 375 g 137 t
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1.052
51.333
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/clone="IMAGE:4154602"
/clone_11b="NCI_CGAP_Brn67"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B (T1 phage-resistant)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="anaplastic oligodendroglioma with 1p/19q/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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Gaps: 5
Percent Identity: 22.000
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483

GACCAGCGCAAAGCGACAGCACAAGAAACAGACACTGGCTACATAAGA

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SOURCE
ORGANISM
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AUTHORS
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                                                                                Align seg 1/1 to reverse of: BF520534
                                                                                                                            US-09-528-682-1 x BF520534/rev
                                                                                                                                                                                          Percent Similarity:
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                                       2 GlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLysAr 18
GGACAAAAGTTCTATGTAGTC...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: debbys@puccini.crl.umn.edu
University of Minnesota name: M277975e
TIGR Sequence name: MTFCV73TK
More information is available at: http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Plant Pathology
University of Minnesota
495 Borlaug_Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST458006 DSIL Medicago truncatula cDNA clone pDSIL-24M2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESTs from leaves of Medicago truncatula after inoculation with Colletotrichum trifolii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fedorova, M., Pierson, B.L., Samac, D.A., H., Ellis, L., Town, C.D., Bowman, C.L., Holt, I.E. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF520534.1 GI:11609217
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Fax: 651 649 5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Deborah A. Samac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medicago
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                                                                                                                                                                                                             Ratio:
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                                                                                                                                                                                                                                                                                                                                          124
                                                                                                                                                                                                                                                                                                                                          Ø
                                                                                                                                                                                                                                                                                                                                                       from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells. Note: EST may be of fungal origin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript SK-; Site_1: ECORI; Site_2: XhOI; cDNA was prepared from polyA+ enriched RNA from cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolli. The cDNA was
                                                                                                                                                                                       80.50
1.750
63.889
                                                                                                                                                                                                                                                                                                                                                                                                                       Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 days after inoculation with Colletotrichum trifolii"
/lab_host="E. coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  directionally ligated into the Uni-ZAP XR vector from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="leaves infected with Colletotrichum
trifolii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Medicago truncatula"

cultivar="genotype A17"

/db_xref="taxon:3880"

/clone="pDSIL-24M2"

/clone_lib="DSIL"
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, Hansen,T.S
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alignment_block:
US-09-528-682-1 x AU209914/rev
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Quality:
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118 yIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyValI 135 :::||||| :::::: ::: |||
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                                                                  390 GGGATTCCATCACCGTACCATCATCAACAACAA.....GA
                                                                                                          102 GlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGlyGl 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 hrGlnMetAsnIle...AsnLeuTyrAspHisAlaArgGlyThrGlnThr 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AU209914 unpublished oligo-capped cDNA library, stage L1 Caenorhabditis elegans cDNA clone yk750d06 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Biology Lab.
Mational Institute of Genetics
Natianal Institute of Jenetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 81-559-81-6854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A complementary view of the C.elegans genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kohara, Y., Shin-i, T., Thierry-Mieg, J.,
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                                                                                                                                                                                                                                                                                                   Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          97
                                                                                                                                                                                                                                                                                                                                                                                                                                          D
                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Hermaphrodite"
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/dev_stage="L1"
/dev_stage="L1"
118 c 154 g 145 t
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/strain="N2"
                                                                                                                                                                                                                                                                           80.50
1.184
49.635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="yk750d06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="unpublished
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                                                                                                                                                                                                                                                                           Length: 137
Gaps: 7
Percent Identity: 24.088
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8

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BASE COUNT
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                                         alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 AAGAACAACGGATCCACCGAGTTCGATCTTACCCAGAAGACCATCACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 leAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyrArg 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 TCTACCGTATTGGAAAGTCTGCTCT......CACTGAGGAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CysAsnGluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGl 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCTCAAGTGGATCGACACCAGTTCCAAGACCGGACACGGTCGCTTCCAA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nSerLysValLysArgGlnIlePheSerAspTyrGlnSerGluValAspI 232
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                  Genome Biology Lab.
Mational Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 81-559-81-6855
Fax: 81-559-81-6855
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A complementary view of the C.elegans genome
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                                                                                                                             101
                                                                                                                                                                                                                                                                                                                                              ykohara@lab.nig.ac.jp
Location/Qualifiers
      80.50
1.184
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123 c 156 g 153 t
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L1"
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LOCUS AU209839
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US-09-528-682-1 x AU222397/rev
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                                                              source
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                                                                                                                   Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 81-559-81-6855
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                           EST.
Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
Eukaryota; Metazoa; Nematoda; Caenorhabditis.
                                                                                                                                                                                                                                        Unpublished (2001
                                                                                                                                                                                                                                                                                                                                                                                                                                            AU209839.1 GI:14845691
                                                                                                                                                                                                                         Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                  and Sugano, S
                                                                                                                                                                                                                                                                                                  Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D.,
                                                                                                                                                                                                                                                             complementary view of the C.elegans
                                                                             ykohara@lab.nig.ac.jp.
Location/Qualifiers
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                                       organism="Caenorhabditis elegans"
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cDNA library, stage
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                                                                                                                                                            Japan
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158

184

272 151

genome

Suzuki, Y

EST 17-JUL-2001

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BASE COUNT
ORIGIN
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KEYWORDS
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      TITLE
                                         AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 ....CATCATGCTTCGTGGAGCCGTTCTCGGACCAAAGAAGCGTCTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 TCTACCGTATTGGAAAGTCTGCTCT...........CACTGAGGAAGGA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 GlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGlyGl 118
                                                                                                                                                                                                                                                                                                                                                                   78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPhePr 168
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                                                                                                                                                                                                                                                                                                                                                                                                        leTyrAsnArg 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nSerLysValLysArgGlnIlePheSerAspTyrGlnSerGluValAspI 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCCTCCGCAAGTCGCTCATCACCCA.....
                                                        Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 571)
                                                                                                                                                              AU215136.1 GI:14853293
EST.
                                                                                                                                                                                                                     AU215136 unpublished oligo-capped Caenorhabditis elegans cDNA clone
A complementary view of the
                  Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D.,
and Sugano,S.
                                                                                                                                                                                                        AU215136
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L1"
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/tissue_type="whole animal"
/dev_stage="L1"
130 c 163 g 159 t
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CDNA library, stage L2
yk821g09 3', mRNA sequence
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                                         Suzuki,Y.
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seq_documentation_block:
LOCUS AU211806
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US-09-528-682-1 x AU215136/rev
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                                                                                     ACCACAGCCGA 55
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 4:
Tel: 81-559-81-6854
Fax: 81-559-81-6855
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Contact: Yuji Kohara
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Location/Qualifiers
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/tissue_type="whole a
/dev_stage="L2"
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/db_xref="taxon:6239"
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US-09-528-682-1 x AU211806/rev
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Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 81-559-81-6854
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 586)
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Contact: Yuji Kohara
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Location/Qualifiers
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/tissue_type="whole animal"
/dev_stage="L2"
137 c 169 g 167 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Sugano, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ykohara@lab.nig.ac.jp
Location/Qualifiers
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Align seg 1/1 to reverse of: AU221819 from: 1
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152 AsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPhePr
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                                                                                                     leAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyrArg
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S99 bp mRNA linear EST 17-JU AU221819 unpublished oligo-capped cDNA library, stage L1 Caenorhabditis elegans cDNA clone yk898e07 3', mRNA sequence. AU221819
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Hermaphrodite"
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/dev_stage="L1"
142 c 172 g 168 t
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@nirs.go.jp
method:uni-directional, sequence direction:sequenced from
(5' -> 3')
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AV399458
                                                                                                                               Quality:
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Bombyx mori cDNA
Unpublished (2000)
Contact: Mita K
                                                                                                                                                                                                                                                                                                                                                                                                            Project='Silkworm Genome Program in MAFF, and Research for the Future Program in JSPS'. see 'SilkBase', <a href="http://www.ab.a.u-tokyo.ac.jp/silkbase/">http://www.ab.a.u-tokyo.ac.jp/silkbase/</a>, for whole ESTdb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Di
; Bombycoldea; Bombycidae; Bombyx.
1 (bases 1 to 608)
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1.342
44.776
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/dev_stage="129 g 154 t
                                                                                                                                                                                                                                                                                                    inoculation"
                                                                                                                                                                                                                                                                                                                   /clone_lib="Bombyx mori
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Caenorhabditis elegans
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Eukaryota; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                               Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 4:
Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                         A complementary view of the C.elegans genome Unpublished (2001)
                                                                                                                                                                                                                                                                                                          Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                               Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AU215966.1 GI:14854123
                                                                                                                                                                                                                                                                                                                                                                and Sugano,S.
                                                                                                                                                                               ykohara@lab.nig.ac.jp.
Location/Qualifiers
/sex="Hermaphrodite"
/tissue_type="whole animal"
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                                                                                                            /db_xref-"taxon:6239"
                                                                                                                         /strain="N2"
                                                                                                                                             ∕organism="Caenorhabditis
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Ratio:
                                                                                                                                                                                                                                                                                                 BJ138457 unpublished oligo-capped cDNA library, C. elegans L1 stage Caenorhabditis elegans cDNA clone ykl135f09 3', mRNA sequence.
   Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Tel: 81-559-81-6856
                                                                                                                                                        Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 634)
Tobase 1 to 634)
                                                                                         A complementary view of the C.elegans genome Unpublished (2002)
                                                                                                                            and Sugano,S.
                                                                                                                                         Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D.,
                                                                                                                                                                                                                                                                     BJ138457.1 GI:18298623
                                                                                                                                                                                                                                                                                                                                         BJ138457
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                  411-8540, Japan
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                                                                                                                                             Suzuki,
ACCESSION
VERSION
KEYWORDS
SOURCE
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US-09-528-682-1 x BJ138457/rev
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Quality:
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ORIGIN
                                                                                      DEFINITION
                                                                                                                       seq_documentation_block:
                                                                                                                                                           seq_name: gb_est1:AU218912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 TCTACCGTATTGGAAAGTCTGCTCT......CACTGAGGAAGGA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 yIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyValI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              448 GGGATTCCATCACCGTACCATCATCAACAACAA......GA
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                                                                                                                                                                                                                                                                                                                                                                       CysAsnGluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGl
                                                                                                                                                                                              ACCACAGCCGA 122
                                                                                                                                                                                                                               leTyrAsnArg 235
                                                                                                                                                                                                                                                                ACCTCAAGTGGATCGACACCAGTTCCAAGACCGGACACGGTCGCTTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                         ACCCTCCGCAAGTCGCTCATCACCCA.............
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oProAspHisGlnAlaTrp......ArgGluGluProTrpIleHisH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGGGAGGATTCCCAAGATACGG.....TATCGTCAACCAGGACTA..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPhePr 168
                                                                                                                                                                                                                                                                                                                                       ... AACCAAGAGAGTCGCCCA.
                                                                AU218912

AU218912 unpublished oligo-capped Caenorhabditis elegans cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-559-81-6855
Email: tshini@genes
 Caenorhabditis elegans
                                    AU218912.1 GI:14857069
                                                      AU218912
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Location/Qualifiers
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/strain="N2"
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49.635
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Gaps:
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                                                                 mRNA linear EST 17-JU CDNA library, stage Ll yk870h06 3', mRNA sequence.
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EST 17-JUL-2001

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REFERENCE
AUTHORS
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US-09-528-682-1 x AU218912/rev
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Ratio: 1.184
Percent Similarity: 49.635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: AU218912 from: 1 to: 639
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                                                                                                                                                                                                                                                                                                                   244 ....CATCATGCTTCGTGGAGCCGTTCTCGGGACCAAAGAAGCGTCTTATC 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 leAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyrArg 151
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336 AAGAACAACGGATCCACCGAGTTCGATCTTACCCAGAAGACCATCACCCC 287
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                                                                         nSerLysValLysArgGlnIlePheSerAspTyrGlnSerGluValAspI 232
                                                                                                                                  isAlaProGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThr 198
                                               ACCTCAAGTGGATCGACACCAGTTCCAAGACCGGACACGGTCGCTTCCAA 94
                                                                                                                                                                                                                                                                                                                                                                                                             AATGGGAGGATTCCCAAGATACGG.....TATCGTCAACCAGGACTA.. 245
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Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 639)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
150 c 179 g 183 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="unpublished oligo-capped cDNA library, stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:6239"
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/strain="N2"
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Gaps: 7
Percent Identity: 24.088
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93 ACCACAGCCGA 83

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OM of: US-09-528-682-1 to: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                    / cgn2_6, / cgn2
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Database sequences: 383533
Database length: 122816752
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Query length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search time (sec): 143.210000
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-Q-/cg02_1/USPTO_spool/US09528682/runat_18062002_082443_7827/app_query.fasta_1.689
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-LOOPEXT=0.000 -OGAPOP-4.500 -QGAPEXT=0.050 -XGAPOP-10.000
-XGAPEXT=0.500 -FGAPOP-6.000 -DELEXT=7.000 -YGAPOP-10.000
-YGAPEXT=0.500 -DELOP-6.000 -DELEXT=7.000 -START=1
-MATRIX-blosum62 -TRANS-human40.cd1 -LIST=100 -DCCALICN=200
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-DEVENTMENTS-1-200 -NORM-CONTRACTOR - NORM-CONTRACTOR - NORM-CON
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5/ptodata/2/1na/5A_COMB.seq:US-08-449-045C-24 +
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na/5B_COMB.seq:US-08-416-496A-5+66
na/5B_COMB.seq:US-08-915-136-5+66
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na/6B_COMB.seq:US-08-818-112-17+66
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S-08-295-660-3+
S-08-484-434C-33+
S-07-927-316A-1+
S-08-460-422-5+
S-09-281-476-18+
S-09-281-481-34-
S-09-189-760-1-
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Ratio: 5.189
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/cgn2_6/ptcdata/2/ina/5A_COMB.seq:US-08-750-007-2 + 59.50 87.43
/cgn2_6/ptcdata/2/ina/5B_COMB.seq:US-08-945-024-1 + 59.50 87.43
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US-09-528-682-1 x US-08-823-120-5
                                                                                                                                                                                                                                     ; NAME/KEY:
; LOCATION:
US-08-823-120-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
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Align seg
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                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (510) 601-2708
TELEFAX: (510 (655-3542
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,00
APPLICATION NUMBER: US 08/256,00
EILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0315.00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Immunogenic Detoxified Mutants of TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their TITLE OF INVENTION: Their Use for the Preparation of Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
                                                                                                                                                                                                                                                                                                                                                          LENGTH: 711 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                          Gaps:
Percent Identity:
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59.50 82.21 6.8e+07

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seq_documentation_block:

Sequence 7, Application Patent No. 6149919
GENERAL INFORMATION:

, Application US/08823120 6149919 Domenighini, Mario

APPLICANT: I APPLICANT: I

APPLICANT: Rappuoli, Rino APPLICANT: Pizza, Mariagrazia TITLE OF INVENTION: Immunogeni TITLE OF INVENTION: Cholera TC TITLE OF INVENTION: Their Use

Immunogenic Detoxified Mutants of Cholera Toxin and of the Toxin Lt, Their Use for the Preparation of V

Their Preparation

and

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-823-120-7

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SnArgIleArgAspGluLeu
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ACAGAATTCGGGATGAATTA
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ACGTTTCCGGAGTCTTATGCCCAGAGGT...AATGAGTACTTCGATAGAG
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NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

STREET: 4560 Hor CITY: Emeryville

4560 Horton Street

Chiron Corporation

California

USA

ADDRESSEE:

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alignment_block:
US-09-528-682-1 x US-08-823-120-7
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; LOCATION:
US-08-823-120-7
                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to:
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NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0315.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEPHONE: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (510) 601-
TELEFAX: (510 (655-35
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LENGTH: 723 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,003
FILING DATE: 11-NOV-1994
                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                  51 GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr
                             84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/823,120 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                             GTACTCAAATGAATATCAACCTTTATGATCATGCAAGAGGAACTCAGACG
gSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyTyrSerThrTyrT||||||||||||||
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seq_documentation_block:
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                                  APPLICATION NUMBER: US/08/435
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAZZA, Richard J.
REGISTRATION NUMBER: 27,657
REFERENCE/DOCKET NUMBER: A-19
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08435605A Patent No. 5874287
                                                                                                                                                                                                              ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIR RECEASE #1.0, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 De Havilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Burnette, W. Neal
APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
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CITY: Thousand Oaks
STATE: California
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                  ENGTH:
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; TOPOLOGY: linear; MOLECULE TYPE: cDNA US-08-435-605A-1
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US-09-528-682-1 x US-08-435-605A-1
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Ratio: 4.814
Percent Similarity: 94.167
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                                         sValLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA 234
                                                                                                                            GluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLy 217
                                                                                                                                                           roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn 200
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alignment_block:
US-09-528-682-1 x US-08-449-045C-1
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; LOCATION:
US-08-449-045C-1
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                                                                                                                                                                                                                                                                                                       Ratio:
Percent Similarity:
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INFORMATION FOR SEQ ID NO: 1:
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                                                                   105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/2
FILING DATE: 06-JUL-1994
ATTORNEY AGENT INFORMATION:
NAME: MAZZA, Richard J.
REGISTRATION NUMBER: 27,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 02-MAY-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Burnette, Neal W.
APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 777 base pairs
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155
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                                                                                                                                      34 lyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThrGlnThr
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CITY: Thousand Oaks
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 24-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                    sArgSerGlyGlyLeuMetProArgGlyHisAsnGluTyrPheAspArgG
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                                                                   GCAGTCAGGTGGTCTTATGCCAAGAGGACAGAGTGAGTACTTTGACCGAG
GTACTCAAATGAATATCAACCTTTATGATCATGCAAGAGGAACTCAGACG
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5. 5770203
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Ratio: 4.814
milarity: 94.167
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Percent Identity:
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alignment_block:
US-09-528-682-1 x
                                                                                                         ; LENGTH: 2020
5223610-1
                                                                                                                                                                                                       seq_documentation_block:
;Patent No. 5223610
; Patent No. 5223610
; APPLICANT: Burton, Frank H.;Sutcliffe, Gregor
;TITLE OF INVENTION: CHOLERA TOXIN GENE REGULATED
                                                                     alignment_scores:
                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5223610-1
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,852
FILING DATE: 18-MAY-1990
SEQ ID NO:1:
                                  Ratio:
Percent Similarity:
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                                                          Quality:
5223610-1
                                  : 1073.00
: 4.790
: 93.333
                                   Percent
                                   Identity:
                                   80.833
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seq_documentation_block:
; Sequence 5, Application US/08435605A
; Patent No. 5874287
                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-435-605A-5
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                                                                  GENERAL INFORMATION:
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APPLICANT: Burnette, W. Neal APPLICANT: Kaslow, Harvey R. TITLE OF INVENTION: RECOMBINATIFLE OF INVENTION: SUBUNIT A NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                        217
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|GCAGTCAGGTGGTCCTATGCCAAGAGGACAGAGTGAGTACTTTGACCGAG
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                                                                                                                                                                                                                                                                                                                    roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn 200
                                                                                                                                                                                                                                                                                                                                                                       eProProAspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaP 184
                                                                                                                                                                                                                                                                                                                                                                                                                            AGTTAAAAGACAAATATTTTCAGGCTATCAATCTGATATTGATACACATA 1269
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                           RECOMBINANT DNA-DERIVED CHOLERA TOXIN
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alignment_block:
US-09-528-682-1 x US-08-435-605A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/435
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAZZA, RICHARD J.
REGISTRATION NUMBER: 27,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
134 alIleAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyr 150
                                          351
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                                                                                                                                                                                                                                                                                                                                                                                        51 GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr 67
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STRANDEDNESS: single
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CITY: Thousand Oaks
STATE: California
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                                                                                                                                                                                                                                                                                                            gSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyTyrSerThrTyrT 84
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                                                                                                                      TTAGGGGCATACAGTCCTCATCCAGATGAACAAGAAGTTTCTGCTTTAGG
                                                                                                                                           LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTACTCAAATGAATATCAACCTTTATGATCATGCAAGAGGAACTCAGACG
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                                                               yGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyV 134
                                                                                                                                                                                                                                                                                       AAGTGCCCACTTAGTGGGTCAAACTATATTGTCTGGTCATTCTACTTATT
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1840 De Havilland Drive
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5.049
95.855
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alignment_block:
US-09-528-682-1 x US-08-435-605A-7
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                                                                                                                                                    Align seg 1/1 to: US-08-435-605A-7
                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application Patent No. 5874287 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,605A
APPLICATION NUMBER: US/08/435,605A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,657
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STATE: California
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LENGTH: 576 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BUTNETTE, W. Neal
APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
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1 AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 05-MAY-
CLASSIFICATION: 435
                                                                           1 AATGATGATAAGTTATATCGGGCAGATTCTAGACCTCCTGATGAAATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
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1840 De Havilland Drive
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5.071
95.833
                                                                                                                                                                                                                                 percent Identity: 86.979
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seq_documentation_block:
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APPLICATION NUMBER: US/08/435,605A FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAZZA, RICHARD J.
REGISTRATION NUMBER: 27,657
REFERENCE/DOCKET NUMBER: A-196B
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08435605A Patent No. 5874287
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Burnette, W. Neal

APPLICANT: Kaslow, Harvey R.

TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN

TITLE OF INVENTION: SUBUNIT ANALOGS

NUMBER OF SEQUENCES: 57
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Amgen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                        STATE: California
COUNTRY: USA
ZIP: 91320-1789
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||||||||||:::||||||
TGGGATTCCATACTCCCAAATATATGGATGGTATCGAGTTCATTTTGGGG 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCCGGGTTGTGGGAATGCTCCAAGA 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       allleAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyr 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGATTTGTTAGGCACGATGATGGATATGTTTCCACCTCAATTAGTTTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTAACTTAGATATTGCTCCAGCAGCAGGTTATGGATTGGCAGGTTT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATATATATGTTATAGCCACTGCACCCAACATGTTTAACGTTAATGATGTA 300
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-435-605A-9
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   Quality:
                                                                                                                                                                                                                                                                                                                               alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5223610-4
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;Patent No. 5223610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5223610-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO:4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-435-605A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-528-682-1 x US-08-435-605A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 18-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 AspThrCysAsnGluGluThrGlnAsnLeuSerThrIleTyrLeuArgGl 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 138 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 uTyrGlnSerLysValLysArgGlnIlePheSerAspTyrGlnSerGluV 230
                                                                                                                                        674 ATTCACGGCGTGGGGAAACAACGAC
                                                                                                                                                                                                        627 GTATACCGCTATGACTCCCGCCCGCCGGAGGACGTTTTCCAGAAC...GG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 TTGATACACATAATAGAATTAAGGATGAATTA 138
                   55 TyrAspAspGlyTyrValSerThrSerLeuSerLeuArg.........
                                                                                                    38
                                                                                                                                                            57 ATACCAATCTAAAGTTAAAAGACAAATATTTTCAGGCTATCAATCTGATA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AATACTTGCGATGAAAAAACCCAAAGTCTAGGTGTAAAATTCCTTGACGA
                                                                                                                                                                                                                          5 LeuTyrArgAlaAspSerArgProProAspGluIleLysArgSerGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4207
                                                                                      Quality:
                                                                    AATGTGCTCGACCATCTGACCGGACGTTCCTGCCAGGTCGGCAGC
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Percent Identity:
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Percent Identity:
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REGULATED BY GROWTH
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seq_documentation_block:
;Patent No. 5244657
; APPLICANT: KLIEN, M
                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5244657-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 isAlaProGlnGly...cysGlyAsnSerSerArgThrIleThr..... 195
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1423 GCAGCCCCTATGGACGCTGCGCGGAACAAGACCCGTGCCCTGACCGTGGCG 1472
                                                                                                                                                                               1534 TATTTGCGCTCTAC 1547
                                                                                                                                                                                                                                                                                                                                                                                                                      1473 GAATTGCGCGGCAGCGGCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 yr.....
                                                                                                                                                                                                                                    222 lePheSerAspTyr 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 TrpTyrArgVal...... 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 LeuGlyValTyrSerProHis......ProTyrG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     888 GACAACAATTTCTACGGCGCCCCCCCCCGTACTTCGAATACGTCGACAC
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                                                                                                                                                                                                                                                                                              .....CTGCAGGAGTACCTGCGTCATGTGACGCGCGGCTGGTCAA 1533
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                                                                                                                                                                                                                                                                                                                                                  rThrIleTyrLeuArgGluTyrGlnSerLysValLysArg.....GlnI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGTAATTGAACAGCATGCCGATCGACCGCAAGACGTCTGCCCCAGGCAT 1387
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KLIEN, MICHEL A.; BOUX, HEATHER A.; COCKLE
                                                                                                                                                                                                                                                                                                                                                                                                                   1493
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alignment_block:
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   Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: 5244657-4 from: 1
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Percent Similarity: 40.271
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1000 TGGCACACCGGCGCATTCCG..........CCCGAAAACATCCGC 1034
                                                                                                                                             155 eAlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProProAspHisG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/589,423
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 275,376
FILING DATE: 23-NOV-1988
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CURRENT APPLICATION DATA:
                                  172 lnAlaTrpArgGluGluProTrpIleHisHisAlaProGlnGlyCysGly 188
                                                                                                   965
                                                                                                                                                                                                                                      141 ArgAsnArgGluTyrArgAspArgTyrTyrArgAsnLeuAsn.....Il 155
                                                                                                                                                                                                                                                                                                         124 leTyrGlyTrpTyrArgValAsnPheGlyValIleAspGluArgLeuHis 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 .....SerAlaHisLeuAlaGlyG 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 AlaProAsnMetPheAsnValAsnAspValLeuGlyValTyrSerProHi 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 yLeuMetProArgGlyHisAsnGluTyrPheAspArgGlyThrGlnMetA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 LeuTyrArgAlaAspSerArgProProAspGluIleLysArgSerGlyGl 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4208
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                                                                                                                                                                                                .....GAATACGTCGACACTTATGGCGACAATGCCGGCCGTATCCT
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seq_documentation_block:
; Patent No. 5433945
; Patent No. 543945
; Patent No. 5450ENCES: 10
; CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/07/979,798
; PILING DATE: 20-NOV-1992
; PRIOR APPLICATION NUMBER: 589,423
; PRIOR APPLICATION NUMBER: 589,423
; PATENT NUMBER: 28-SEP-1990
    APPLICATION NUMBER: 275,376
; PATENT DATE: 23-NOV-1988
; SEC ID NO.4.
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US-09-528-682-1 x 5433945-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , LENGTH: 4208
5433945-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1085 GGAGTATTCCAAC 1097
                                                                                                  107
                                                                                                                                                                                                                                                                                                                                                                                                                                            744 AGCAACAGCGCTTTCGTCTCCACCAGCAGCCGGCGCGCTATACCGAGGT 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    674 ATTCACGGCGTGGGGAAACAACGAC......698
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                                                                                                                                                                                                                                                                                                                                           794 CTATCTCGAACATCGCATGCAGGAAGCGGTCGAGGCCGAACGCGCCGCA 843
124 leTyrGlyTrpTyrArgValAsnPheGlyValIleAspGluArgLeuHis 140
                                                                                                                                                                                                                                              844 GGGGC.....ACCGGCCACTTCATCGGCTACATCTACGAAGTC...CGC 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         699 ....AATGTGCTCGAACATCTGACCGGACGTTCCTGCCAGGTCGGCAGC 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       627 GTATACCGCTATGACTCCCGCCCGCCGGAGGACGTTTTCCAGAAC...GG
                                                                                                                                                                                                   91
                                                                                                                                                                                                                                                                                           74 lnSerIleLeuSerGlyTyrSerThrTyrTyrIleTyrValIleAlaThr 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 snIleAsnLeuTyrAspHisAlaArgGlyThrGlnThrGlyPheValArg 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 LeuTyrArgAlaAspSerArgProProAspGluIleLysArgSerGlyGl 21
                                                                                                                                                                                                AlaProAsnMetPheAsnValAsnAspValLeuGlyValTyrSerProHi 107
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                                                                                             sProTyrGluGlnGluValSerAlaLeuGlyGlyIleProTyrSerGlnI 124
                                                                                                                                             GCCGACAACTTC..... 899
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1.000
40.271
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Percent Identity:
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11
23.529
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alignment_block:
us-09-528-682-1 x us-09-103-840A-1/rev
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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: US-09-103-840A-1 from: 1 to: 4411529
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3735464TCGCTCGGCGTCGGCATACCCAATATTTCGATCGGCCCCATCAA..... 3735421
                                                                                                                                                                                                                                                                                                           3735564TATCGAGCCCATCCACATACTTCCCGACATCCCGATCAACATCAACGAAA 3735515
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM FILE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1035 AGGGTAACGCGGGTCTATCACAACGGCATCACCGGCGAGACCACGACCAC 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1085 GGAGTATTCCAAC 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1000 TGGCACACCGGCGCATTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 uGluThrGlnAsn 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 lnAlaTrpArgGluGluProTrpIleHisHisAlaProGlnGlyCysGly 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         965 CGCCGGCGCG......CTGGCCACCTACCAGAGCGAATATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             900 ..TACGGCGCCGCCAGCTCGTACTTC............
                                  39 IleAsnLeuTyrAspHis...AlaArgGlyThrGlnThrGlyPheValAr 54
                                                                                                                               22 euMetProArgGlyHisAsnGluTyrPheAspArgGlyThrGlnMetAsn 38
                                                                                                                                                                                                                                                   6 TyrArgAla......AspSerArgProProAspGluIleLysArgSe 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .......GAATACGTCGACACTTATGGCGACAATGCCGGCCGTATCCT 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.50
1.086
37.826
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Percent Identity:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS TITLE OF INVENTION: AND NUCLEIC ACID SEQUENCES CODING THEREFOR FILE REFERENCE: CGC1963/A CURRENT APPLICATION NUMBER: US/09/251,645 CURRENT FILING DATE: 1999-02-17 NUMBER OF SEQ ID NOS: 22 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1
LENGTH: 9717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3735348CATAACAATTCCCCAAATCCAACAGGTCGCCCTCAGCCCTTCCCCCCATTC 3735299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09251645 Patent No. 6281413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Warren, Gregory W. APPLICANT: Dunn, Martha APPLICANT: Chen, Jeng S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Anderson, Arne R. APPLICANT: Hart, Hope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kramer, Vance C. APPLICANT: Morgan, Michael K.
                                                                                                                           NAME/KEY: CDS
LOCATION: (412)...(1665)
OTHER INFORMATION: orf1 ~46.4 kDa
LOCATION: (1686)..(2447)
OTHER INFORMATION: orf2 ~28.1kDa
                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                  ORGANISM: Photorhabdus luminescens
                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                    NAME/KEY: CDS
                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 lAsnPheGlyValIleAspGluArgLeuHisArgAsnArgGluTyrArgA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 LeuAlaGlyPheProProAspHisGlnAlaTrpArg.GluGluProTrpI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 spArgTyrTyrArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArg 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 SerAlaLeuGlyGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgVa 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 gTyrAspAspGlyTyrValSerThrSerLeuSerLeuArgSerAlaHisL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leHisHisAlaProGlnGlyCysGlyAsnSerSerArg 192
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seq_documentation_block:
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US-09-528-682-1 x US-09-251-645-1
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                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08296848A Patent No. 6019982
                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (4515)..(9269)
OTHER INFORMATION: orf5
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NAME/KEY: CDS
LOCATION: (2758)..(3318)
OTHER INFORMATION: orf3 ~20.7 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (3342)..(4118)
OTHER INFORMATION: orf4 ~28.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8397 CAGGTTGATCCAGTAACAGGCTGGTACTTCTTAGGTAACGGA 8438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8347 CTTATGGCTTTAGGAGTTTAATTTCCTCATTACCGGGTTTGAATGGCGCA 8396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8199 ..ATTACTTGGTTGAGCAGTGATAAGCAACGAATTGGACATCAAAGCGCC 8246
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106
                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                       APPLICANT: Clements, John D. APPLICANT: Dickinson, Bonny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 Gln......IleTyrGlyTrpTyrArgValAsnPheGly 133
                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 alSerThrSerLeuSerLeuArgSerAlaHisLeuAlaGlyGlnSerIle 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 pHisAlaArgGlyThrGlnThrGlyPheValArgTyrAspAspGlyTyrV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 HisAsnGluTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAs 43
                                                                                                 STREET: 1155 ACCITY: New York
STATE: New York
                                                COUNTRY: U.S.A. ZIP: 10036
                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         roHisProTyrGluGlnGluValSerAlaLeuGlyGlyIleProTyrSer 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rAlaProAsnMetPheAsnValAsnAspValLeuGlyVal...TyrSerP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuSerGlyTyrSerThrTyrTyrIleTyrValIle.....AlaTh 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                 New York
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                                                                                                                                               1155 Avenue of the Americas
                                                                                                                                                                  PENNIE & EDMONDS LLP
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1.419
54.386
                                                                                                                                                                                                                                      n, Bonny L.
MUTANT ENTEROTOXIN EFFECTIVE AS
NON-TOXIC ORAL ADJUVANT
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Percent Identity: 26.316
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CURRENT APPLICATION DATA:

PatentIn Release #1.0,

Version

US/08/296,848A

PC-DOS/MS-DOS

OPERATING SYSTEM: SOFTWARE: Patent:

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seq_documentation_block:
; Sequence 9, Application
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-204-656B-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: US-08-296-848A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-296-848A-1 from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-528-682-1 x US-08-296-848A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
ATTORNEY/AGENT INFORMATION:
NAME: Welher, MAIC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Oligosaccharide Using The Enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 GlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn 200
                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 26-AUG-1994 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGTTGTGGAAATTCATCAAGAACAATTACAGGTGATACTTGTAAT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                             FILING DATE: 0: CLASSIFICATION:
                                                                                                APPLICATION NUMBER: US/08/204,656B FILING DATE: 02-MAR-1994
                                                                                                                                                                                                                                                                                                                  CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                         22042
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EDNESS: double
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Y: U.S.A.
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                                                                                                                                                                                                                                                                                                                                 8110 Gatehouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ishikawa, Kazuhiko
Miyairi, Sachio
Honda, Koichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matsui, Ikuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (212) 869-8864/9741
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5.733
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nouse Road, Suite 500 East
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    234-252P
                                                                                                                                                         Version #1.30
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alignment_block:
US-09-528-682-1 x US-08-204-656B-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                             505
                                                                                                                                                                                                                                                                                                                                                                                  484
                                                                                                                                                                                                                                                                                                                                                                                                                                                            449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 AGGTCGGATCGACTTCGCCCCCAACCACAC......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic
620 TGGACGCTTATTTTAAAAGCGCTATCGACCTTTGGCTCGGCATGGGTGTG
                                                                                                                                                                                                                                                                                                     501 CAGC....
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TELEFAX: 248345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 lyPheValArg......TyrAspAspGlyTyrValSerThrSer 63
                                                                                                                                                                                                                                                               97 alAsnAspValLeuGlyValTyrSerProHisProTyrGluGlnGluVal 113
                                                                                                                                                                                                                                                                                                                                                                                                                    64 LeuSerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 yThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThrGlnThrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 ArgSerGlyGlyLeuMetProArgGlyHisAsnGluTyrPheAspArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..2061
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2061 base pairs
                                                                                                         gValAsnPheGlyValIleAspGluArgLeuHisArgAsnArgGluTyrA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTTCGCCGAGAACGGTGCGCTGTATGATAACGGT......
                               rgAspArgTyrTyrArg......AsnLeuAsnIleAlaProAlaGlu 159
                                                                         GAACCTCTACGACCTGGCGGAC....ATCAACCATAACAACAACGCTA
                                                                                                                                                                                   SerAlaLeuGlyGlyIleProTyrSerGlnIleTyr...GlyTrpTyrAr 129
                                                                                                                                                                                                                           rSerThrTyrTyrIleTyrValIleAlaThrAlaProAsnMetPheAsnV
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                                                                                                                                                   ........GGGGGGACCGATTTTTCCACGATTGAAGACGGTATTTACAA 575
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Library of chromosomal DNA from Bacillus macerans, pMAC, generated by treating chromosomal DNA from Bacillus IAM1243 with a restriction enzyme, and inserting and linking restric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragments to pBR322
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0.852
40.664
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13
21.577
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-470-702-5
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                                                                                                                       TELEX: 248345
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                  APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 25-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160
                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: UFILING DATE: 06-JUN-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        720 AAGCTTCGTTTCCTCGATTTACGGCGGCGATCATCCGGTATTTACGTTCG 769
  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                               TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 8110 Gateho
CITY: Falls Church
                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACGGGATTCGTTTGACGGGGTGAAGCAGTATCCTTTCGGCTGGCAAAA 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....TTCGCCAACGAAAGCGGGATGAACCTGCTGGACTTT.. 852
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                                                          nucleic acid
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                                                                              2061 base pairs
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MIYAIRI, SACHIO
HONDA, KOICHI
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                       linear
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DNA (synthetic)
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alignment_block:
US-09-528-682-1 x US-08-470-702-5
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                                                                              817
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                                                                                                                                                                                                                                         720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 ArgSerGlyGlyLeuMetProArgGlyHisAsnGluTyrPheAspArgGl 34
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                                                                                                                                                                                                                                                                                                                                                       rgAspArgTyrTyrArg......AsnLeuAsnIleAlaProAlaGlu 159
                        rLeuArgGluTyrGlnSerLysValLysArgGlnIlePheSerAsp...T 226
                                                                                                                 IleThrGlyAspThrCysAsnGluGluThrGlnAsnLeuSerThrIleTy
                                                                                                                                                           GGGAATGGTATCTTGGCGCGGGATCAAACCGACGGAGACAACATTAAA... 816
                                                                                                                                                                                                                                         AAGCTTCGTTTCCTCGATTTACGGCGGCGATCATCCGGTATTTACGTTCG 769
                                                                                                                                                                                                                                                                                                                      GACGGGATTCGTTTTGACGGGGTGAAGCAGTATCCTTTCGGCTGGCAAAA 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAACCTCTACGACCTGGCGGAC....ATCAACCATAACAACAACGCTA
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.....GAATACGCGCAGGAAGTG...CGCGAAGTGTTCCGGGACAAAA 892
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                                                                            ....TTCGCCAACGAAAGCGGGATGAACCTGCTGGACTTT..
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Ratio:
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Gaps:
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226

yrGlnSerGluValAspIleTyr 233

893 CGGAAACGATGAAGGATCTCTAT 915

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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
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HYPOTHETICAL: N
ANTI-SENSE: NO
US-08-467-831-5
                                                                                                                                                                                alignment_block:
US-09-528-682-1 x US-08-467-831-5
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                                                                                                                                                 Align seg 1/1 to: US-08-467-831-5
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COMPATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIN Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,831
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: MATSUI
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 23:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,
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                                                                             391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
421 .....
                                  34 yThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThrGlnThrG 51
                                                                                                  ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: doub
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5. 5635378
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ISHIKAWA, KAZUHIKO
MIYAIRI, SACHIO
HONDA, KOICHI
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Gaps: 13
Percent Identity: 21.577
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	MEDIUM TYPE: F1	
	4111-41 READARI	
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,	: 4 Embarcadero Center, Suite 3400 San Francisco	** ** *
	DENCE ADDRESS: EE: Flehr, Hohbach, Test, Alb	
	TITLE OF INVENTION: PROGRAMMED CELL DEATH ANTAGONIST TITLE OF INVENTION: PROTEINS NUMBER OF SEQUENCES: 8	
	CANT: Bonini, Nancy CANT: Leiserson, Wi	
	<pre>sq_documentation_block: Sequence 1, Application US/08195152 Patent No. 5679541 GENERAL THEORMATION:</pre>	Pa Se Pa
	name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-195-152-1	seq_n
	226 yrGlnSerGluValAspIleTyr 233 	
892	G G	_
226	alLysArgGlnIlePheSerA	
852	817TTCGCCAACGAAGCGGGATGAACCTGCTGGACTTT	_
210	erThrI	
816	770 GGGAATGGTATCTTGGCGCGGGATCAAACCGACGAGACAACATTAAA	
193	roGlnGlyCysGlyAsn	
769	0 AAGCTTCGTTTCCTCGATTTACGGCGCGATCATCCGGTATTTAC	
177	spH	
719	TO ASPOLYTYTATGLEMALEGLY	
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, 5	46 rgAspArgTyrTyrArgA	
619	576 GAACCTCTACGACCTGGCGGACATCAACCATAACAACGACGCTA	
146	llleAspGluArgLeuHisArgAsnArgG	
575	ACCGATTTTCCACGATTGAAGACGGTATTTA	
129	yrSerGlnIleTyrGlyTrpTyrA	
534	505AATGATACGGCCGGCCTTTTCCATCATAAC	
113	spValLeuGlyValTyrSerProHisProTyrGluGlnGluVal	
504	 501 CAGC	
97	SerThrTyrTyrIleTyrValIleAlaThrAlaProAsnMetPheAsnV	
500	64 LeuSerLeuArgSerAlaHisLeuAlaGLYGINSerILEUSerGLYTYP 64 LeuSerGelTeUSerGLYTYP 65 1	
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63 483	rValSerThrSer	

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1151
                                                                                                                                                                                                                                                                                                                                                            1191
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 3231 base pairs
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/OFILING DATE: 14-FEB-1994
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CAGCTGTACAGCAGTCCGTACGCCGGCTACAACAACTTCGGGCAGCAGGA 1402
                                    GlnIleTyr.....
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                                                                                                                                                                                                                                                                                                                                                       .....AACAGCATGCAGCAGTACACGCCG 1214
                                                                                                                                                                                                                                                                                                                                                                                                   hrAlaProAsnMetPheAsnValAsnAspValLeuGlyValTyrSerPro 106
                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCAGCGGTCTACGACGGCAAACATGACTACTACTACTAC.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGGAGCAGTGGCGGTCAACTCTTCGGCAGTGGCAGCG.....GCAGC 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AspGlyTyrValSerThrSerLeuSerLeuArgSerAlaHisLeuAlaGl 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        snLeuTyrAspHisAlaArgGlyThrGlnThrGlyPheValArgTyrAsp 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tProArgGlyHisAsnGluTyrPheAspArgGlyThrGlnMetAsnIleA 40
                                                                                                                                                                                                                                                                    CCGCCCTTCTACTCCGGATAC...........GGAACTCCTTATGCGGC 1252
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Ratio:
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0.833
36.803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                 20.818
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                                                                                                                                 Ser 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1190
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seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US96-05611A-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 28, Application PC/TUS9605611A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1403
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APPLICANT:
TITLE OF IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1653 GTGTCCGCGGCAGCTGCGGCCGCTGCTCAACTCGAGCGGAGGCAGCAG 1702
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                                                                                                   APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                                                                  COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 nIleAla......ProAlaGluAspGlyTyrArgLeuAla.Gly 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139
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                                                         ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                              FILING DATE: 0
CLASSIFICATION:
                  NAME: Klee, Maurice M. REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTACGGCGGCTACTACAACGAGCAGTACGGCAACTATTACAGTCCGGCCA 1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....CysGlyAsnSerSerArgThrIleThrGlyAspThr 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....GluGluProTrpIleHisHisAlaProGlnGly....
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T: Squinto, Stephen P.
T: Wilkins, James A.
INVENTION: Modified Myelin Protein Molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Connecticut
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Nye, Steven H.
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Matis. Toute
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Lenardo. Michael
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02-MAY-1995
                    ALX-129
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TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1476 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: MMOGP4 chimera
HYPOTHETICAL: No
ANTI-SENSE: No
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US-09-528-682-1 x PCT-US96-05611A-28
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Quality:
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Percent Similarity:
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                                                                                                                                                                                                          646
                                                                                                                                                                                                                                                                                                                                                                                                     81 rThrTyrTyrIleTyrValIleAlaThrAlaProAsnMetPheAsnValA 98 :::||| | |||:::::|||:::||| 579 G......ATGGCTAGACGTCCCCGGCAGTTCAGAGTG. 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             743
                                  139 euHisArgAsn............ArgGluTyrArg 146
                                                                                                                                122 rGlnIleTyrGlyTrpTyrArgValAsnPheGlyValIleAspGluArgL 139
                                                                                                                                                                                                                                                    115 AlaLeuGlyGlyIlePro......TyrSe 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            529 TTGTCCAAAATTTTCAAACTGGGCGGCCGTGATAGCCGTTCTGGCTCTCC 578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 ANAGGCCGTGGCCTGTCCCTGAGCCGTTTCAGCTGGGGCGCGCGAAGGCCA 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 CCTGCCGCAGAAATCCCACGGCCGTACCCAGGATGAAAACCCGGTGGTGC 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 ATGTACAAA...GACTCCCACCACCGGGCTCGTACCGCGCACTATGGCTC 293
                                                                                                                                                                                                                                                                                                                                                      98 snAspValLeuGlyValTyrSerProHisProTyrGluGlnGluValSer 114
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                                                                                                                                                                                                       GATGAAGTGGAATTGCCATGTCGCATATCTCCTGGGAAGAACGCTACAGG 695
TCTACAGAAATGGCAAGGACCAAGATGGAGACCAGGCACCTGAATATCGG
                                                                                                   CATGGAGGTGGGTACCGCCCCCCCTTCTCTAGGGTG...GTTCATC 742
                                                                                                                                                                                                                                                                                                         .....ATAGGACCAAGACACCCTATCCGGGCTCTGGTCGGG 645
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0.624
40.439
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Gaps: 16
Percent Identity: 20.063
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1 6	
889	
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934	
183	GlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysA 200
981	GACCTATTTCTCCAAAA
200 1031	snGluGluThrGlnAsnLeuSerThrIleTyrLeuArgGlu
214 1081	TyrGlnSerLysValLysArgGlnIlePheSerAspTyrGlnSe 228
228 1131	rGluVal 230 : ::: CACCATC 1137
seq_name:	: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-449-045C-23
eq_documen Sequence Patent No GENERAL APPLIC	entation_block: 23, Applicati No. 5770203 L INFORMATION: CRANT: Burnett
APPLIC TITLE TITLE NUMBE	CANT: Kaslow, Harvey OF INVENTION: RECOMB OF INVENTION: SUBUNI R OF SEQUENCES: 34
AI SI	RESSEE: Amgen
ខ្លួន	Thousand (Californ: Y: USA
COME	1789 BLE FORM:
	SYSTEM: PC-DOS/MS-DOS
CURF	CATION DATA:
FA	BER:
PRIOR	APPLICATION: 424 APPLICATION DATA:
PRIOR	ING DATE: 02-MAY-1991 APPLICATION DATA:
3	LICATION NUMBER: ING DATE: 06-JUL
2 R R :	Mazza, Richard J. RATION NUMBER: 27,65
INFORA	ION FOR SEQ ID NO: 23:
35	LENGTH: 50 base pairs TYPE: nucleic acid

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; STRANDEDNESS: Sit; TOPOLOGY: linear; MOLECULE TYPE: CDNJ
alignment_block:
                                                                                           alignment_scores:
                                                                                                                                                   US-08-449-045C-24
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                                    Percent Similarity:
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                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: A INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07
FILING DATE: 02-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 06-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Re-lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,045C
FILING DATE: 24-MAY-1995
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 TrpIleHisHisAlaProGlnGlyCysGlyAsnSerSerArgThr 193
                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Burnette, Neal W. APPLICANT: Kaslow, Harvey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                             TYPE:
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                                                                                                                                                                                                    STRANDEDNESS: single
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Ratio:
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F: 1840 De Havilland Drive
Thousand Oaks
                                                                                                                                                                                                                         nucleic acid
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5.714
93.333
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93.333
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                                                                                                                                                                                                                                                                                                                                                                                               US 08/271,222
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                             Length: 15
Gaps: 0
Percent Identity: 80.000
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6
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alignment_scores:
Quality:
Ratio:
                                                                                                               seq_documentation_block:
                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-435-605A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/43
FILING DATE: 05-WAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAZZA, Richard J.
REGISTRATION NUMBER: 27,657
REFERENCE/DOCKET NUMBER: A-1
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                Align seg 1/1
                                                                                                                                                                                                                                                                                                     US-09-528-682-1 x US-08-435-605A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-528-682-1 x US-08-449-045C-24
                                                                          Patent No.
                                                                                              Sequence 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 35,
                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 1in MOLECULE TYPE: DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 91320-1,...
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
medium Type: BM PC compatible
computible
compatible
compatible
APPLICANT: Burnette, W. Neal APPLICANT: Kaslow, Harvey R. TITLE OF INVENTION: RECOMBIN
                                                                                                                                                                                                         179 TrpIleHisHisAlaProGlnGlyCysGlyAsnSerSerArgThr 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Burnette, W. Neal APPLICANT: Kaslow, Harvey R. APPLICANT: Kaslow, Harvey R. TITLE OF INVENTION: SUBUNIT /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 TrpIleHisHisAlaProGlnGlyCysGlyAsnSerSerArgThr 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                      TGGATTCATCATGCACCGCAGGGTTGTGGGAATGCTCCAAGATCA 47
                                                                              5874287
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                                                                                              Application US/08435605P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: US-08-449-045C-24
                                                                                                                                                                                                                                                                  to: US-08-435-605A-35
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1840 De Havilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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/desc = "oligonucleotide"
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5.714
93.333
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 RECOMBINANT DNA-DERIVED CHOLERA TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/435,605A
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Percent Identity:
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TITLE OF INVENTION: SUNUMBER OF SEQUENCES: 5

SUBUNIT ANALOGS 57

ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,657

A-196B

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY: USA ZIP: 91320-1789

ADDRESSEE: Amgen Inc.
STREET: 1840 De Havilland
CITY: Thousand Oaks
STATE: California

Drive

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE:

PatentIn Release #1.0, Version

#1.30

US/08/435,605A

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APPLICANT: Caughey, Bruce W
APPLICANT: Chabry, Joelle
APPLICANT: Priols, Susette
TITLE OF INVENTION: Inhibitors of Formation of
FILE REFERENCE: 50121
CORRENT APPLICATTON:
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US-09-528-682-1 x US-08-435-605A-36
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Quality:
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; DESCRIPTION:
US-08-435-605A-36
                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-128-450-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-435-605A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                              CURRENT APPLICATION NUMBER: US/09/128,450
CURRENT FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 1000
                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/09128450 Patent No. 6211149
NAME/KEY: CDS
LOCATION: (60)..(824)
-09-128-450-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: A INFORMATION FOR SEQ ID NO: 36:
                                                                ORGANISM: Hamster sp.
                                                                                   TYPE: DNA
                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 TrpIleHisHisAlaProGlnGlyCysGlyAsnSerSerArgThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      3 TGGATTCATCATGCACCGCAGGGTTGTGGGAATGCTCCAAGATCA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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STRANDEDNESS: sing
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/desc = "oligonucleotide"
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alignment_scores:

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; NAME/KEY: CDS
; LOCATION: (60)..(824)
US-09-823-494-25
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                                                                                                                                                        NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver.
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6355610 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/09823494 Patent No. 6355610
                                                                                                                                                                                                                                                                                                                    APPLICANT: Chesebro, Bruce W
APPLICANT: Caughey, Byron W
APPLICANT: Chabry, Joelle
APPLICANT: Priola, Susette
TITLE OF INVENTION: Inhibitors of Formation of Protease Resistant Prion
TITLE OF INVENTION: Protein
FILE REFERENCE: 50121
                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/823,494
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/128,450
PRIOR FILING DATE: 1998-08-03
                                                                  TYPE: DNA
ORGANISM: Hamster
FEATURE:
                                                                                                                                        LENGTH: 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            713 TCAGAAGGAGTCCCAGGCCTAC 734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                499 ACCGCTACTACCGTGAAAACATGAACCGCTACCCTAACCAAGTGTATTAC
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Percent Identity:
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alignment_block:

Percent Similarity:

Quality:

Ratio:

80.00 1.176 54.839

Align seg 1/1 to: US-09-823-494-25 US-09-528-682-1 x US-09-823-494-25

417 GCCGTGGTGGGGGGCCTT......

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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-728-603-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cesarman, Ethel
APPLICANT: Knowles, Daniel M.
APPLICANT: KNOwles, Daniel M.
TITLE OF INVENTION: PROTEINS OF KAPOSI'S SARCOMA ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                622 CAGTCACCACCACCAAGGGGGGAG.....AACTTCACGGAGACC 662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: NIXON, HARGRAVE, DEVANS & Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 24.194
                                 19603/720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVANS & DOYLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
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                                                                                                                                                                                                                                                                   Version
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                                                                                                                                                                                                                                                                   #1.30
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Quality:
Ratio:
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US-09-528-682-1 x US-08-728-603-14/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 716-263-1000
TELEFAX: 716-263-1000: 14
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 4332 base pairs
TYPE: nucleic acid
TYPE: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: US-08-728-603-14 from: 1
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                                                                                                                                                                                                                                     3479 TGTATGGTGAGGATTCCGACCGGCCCACTACACCCAGGGCCCACCAGCAGC 3430
                                                                                                                                                                                                                                                                                                                                                   ::;|::::
3520 CAGGTTTACCGCCCAGCGCTGGGGTGGTGGGTCCGTAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3561 TTTAGCCAG.....TGGCTGTCATACAGCTTGGACACGTTGGTCTC 3521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3658 CCGGACCCCCAGGTACTCTCCCTGGGCCCAGCT...GGGCAGCACCGTCC 3612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3758 AGTGTCTGGCTGGCAGGGTCTCATCCGCGGCATTTCCATGGTAGGTGAGG 3709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3808 ACTGGATGTAAGTCCGGCCACCGTGGAGTTGCCTGTGGGGTTTCTGGGAT 3759
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                                                                                                                                                                                                                                                                                                                                                                                                             137 uArgLeuHisArgAsnArg......GluTyrArgAspArgT 149
                                                                                                                                                                                                                                                                                      149 yrTyrArg.AsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAl 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyValIleAspGl 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 erIleLeuSerGlyTyrSerThrTyrTyrIle.....TyrValIleAla 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 rPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
AAACTCTGTCAGGGTGGAGGCACAGGTAGGGTCGTTACACAGCGCCAGGA 3330
                                                TGGAAGCCCACCTCGCCACAGCAGATGGAGAATGTGTCGGGTCTGTTTAG 3380
                                                                                                                                                                        aGlyPheProProAspHisGlnAlaTrpArgGlu.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTATCTCGCCTCGCTGTCTCAGTATGTACTCGAGGGCGTCCTGCTCGTA 3659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....LeuAlaGlyGlnS 75
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0.630
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Sequence 14, Application US/08728603 Patent No. 6093806

_documentation_block:

713 TCAGAAGGAGTCCCAGGCCTAC 734

rGlnSerGluValAspIleTyr 233

179 549 163 499 147 449

to: 4332

193

GENERAL INFORMATION:

APPLICATION NUMBER: US/08/728
FILING DATE: 10-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BRAWAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 1960

TELECOMMUNICATION INFORMATION:

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:

US/08/728,603

COMPUTER READABLE FORM:

COUNTRY:

USA

14603

MEDIUM TYPE:

Floppy disk

....G 3480

STREET: CIL...
CTTY: Rochester
''Ou York

CORRESPONDENCE ADDRESS:

ADDRESSEE:

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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5234:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-379-20
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Patent No. 5849564
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
                                                                                                                                       alignment_block:
US-09-528-682-1 x US-08-770-379-20
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                                                                                                                                                                                                           Quality:
Ratio:
Percent Similarity:
                                                                                              Align seg 1/1 to: US-08-770-379-20
3329 CCCATCCCCTGGCGCTGGCGTAGCTGGCCTGGCAGCCTGTTCTGAGACAT 3280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3229 CACAGTCACCGTGGCCACCTCAAAGCCCGTGTT 3197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3279 GTAATCAGACCAGAGAACCCCGACAAGGACTGTCCTCGTTTAAGCTCTTC 3230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER RÉADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 ArgGluTyrGlnSerLysValLysArgGlnIle 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1185 AVER CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10036
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1185 Avenue of the Americas
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0.630
48.289
                                                                                                                                                                                                      Length: 263
Gaps: 18
Percent Identity: 23.194
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                                                                                              from: 1 to: 32207
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VIRUS	Sequence 20, Application US/0875/669A Patent No. 6183751 GENERAL INFORMATION: APPLICANT: Chang, Yuan APPLICANT: Russo, James J. APPLICANT: Edelman, Isidore S. APPLICANT: Edelman, Isidore S. APPLICANT: BOOFE, PATRICKS S. TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA
õ	_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-757-669A-2 _documentation_block:
	212 ArgGluTyrGlnSerLysValLysArgGlnIle 222 ::::::::::::::::::::::::::::::::::
211 25993	199 ysasnGluGluThrGlnAsnLeuSerThrIleTyrLeu
199 25943	185 nGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrC : ::::: ::: ::::: ::: 25894 CCCATCCCCTGGCGTGGCGTAGCTGGCAGCCTGGCAGCCTGTTCTGAGACAT
185 25893	177GluProTrpIleHisHisAlaPro.Gl :::
176 25843	165 aGlyPheProProAspHisGlnAlaTrpArgGlu
165 25793	149 yrTyrarg.AsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAl
149 25743	137 uArgLeuHisArgAsnArgGluTyrArgAspArgT
137 25702	121 TyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyValIleAspGl::::
120 25661	106 oHisProTyrGluGlnGluValSerAlaLeu.GlyGlyIlePro
106 25611	90 ThralaProAsnMetPheAsnValAsnAspValLeuGlyValTyrSerPr :::::::::::::::::::::::::::::::::
89 25564	75 erileLeuSerGlyTyrSerThrTyrTyrIleTyrValileAla ::: ::::::
75 25514	71LeualaGlyGlnS ::::::: :::: 25465 AGTGTCTGGCTGGCAGGGTCTCATCCGCGGCATTTCCATGGTAGGTGAGG
70 25464	64 LeuSerLeuArgSerAlaHis
63 25414	47 lyThrGlnThrGlyPheValArgTyrAspAspGlyTyrValSerThrSer :::
47 25367	30 rPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgG

TITLE OF INVENTION:

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alignment_block:
US-09-528-682-1 x US-08-757-669A-20
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                                                                                                                                                                                                                                                                                                                                                                        25328
25565 CCGGACCCCAGGTACTCTCCCTGGGCCCAGCT...GGGCAGCACCGTCC 25611
                                                                                                                                               25465 AGTGTCTGGCTGGCAGGGTCTCATCCGCGGCATTTCCATGGTAGGTGAGG 25514
                                                                                                                                                                                                                      25415 ACTGGATGTAAGTCCGGCCACCGTGGAGTTGCCTGTGGGGTTTCTGGGAT 25464
                                                                                                                                                                                                                                                                                               25368 TGGAACATCAGAGATGGGTC...TATGATCAGGGCAGCGTGTCGCCCGTC 25414
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INFORMATION FOR SEQ ID NO: 2
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 424
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LENGTH: 32207 base pai
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45
                                                                                                               75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                90 ThrAlaProAsnMetPheAsnValAsnAspValLeuGlyValTyrSerPr 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 rPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgG 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
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                                                                     GTTATCTCGCCTCGCTGTCTCAGTATGTACTCGAGGGCGTCCTGCTCGTA 25564
                                                                                                         erIleLeuSerGlyTyrSerThrTyrTyrIle....TyrValIleAla 89
                                                                                                                                                                                                                                                         LeuSerLeuArgSerAlaHis.....
                                                                                                                                                                                                                                                                                                                  OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                    ...GGGTGTTAGGTCTGGTGGAACATGCTGCCACTGCCACGGA 25367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Percent Identity: 23.194
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alignment_block: us-09-528-682-1 \times us-09-230-371A-20
                                                                                                                                                                                                                                                ; TYPE: DNA; CAPOSI'S sarcoma-associated herpesvirus US-09-230-371A-20
                                                                                                                                                                               alignment_scores:
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                                                                                                               Ratio:
Percent Similarity:
Align seg 1/1 to: US-09-230-371A-20
                                                                                                                                                                                                                                                                                                                 SEQ ID NO 20
LENGTH: 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6348586
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20,
                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: 45185-G-PCT-US CURRENT APPLICATION NUMBER: US/09/230,371A CURRENT FILING DATE: 1999-11-17 PRIOR APPLICATION NUMBER: PCT/US97/13346
                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
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Moore, Patrick S
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Russo, James
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-296-848A-4
                                                                                                Sequence 4, Application US/08296848A Patent No. 6019982
                                                                                                                                                                                                                                                  25994 CACAGTCACCGTGGCCACCTCAAAGCCCGTGTT 26026
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APPLICANT: Clements, John D. APPLICANT: Dickinson, Bonny TITLE OF INVENTION: MUTANT I
                                                                                                                                                                                                                                                                                                   212 ArgGluTyrGlnSerLysValLysArgGlnIle
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n, Bonny L.
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-296-848A-4 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/07849438 Patent No. 5459034
                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: TABAQCHALI
TITLE OF INVENTION: C.
NUMBER OF SEQUENCES: 2
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                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
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OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the A
                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: 31 Research Exploitation Limited
STREET: The Gate House, 2 Park Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
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NUMBER OF SEQUENCES:
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CITY: New York
STATE: New York
                                                                                                                                                                                                                          STREET: The Ga
CITY: Windsor
STATE: Berkshi
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APPLICATION NUMBER:
                                                                                                                                                                              ZIP: SL4 1LU
                                                                                                                                                                                              COUNTRY: U.K.
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STRANDEDNESS: double
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REFERENCE/DOCKET NUMBER: 51
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  US/07/849,438
                                                                                                                                                                                                                                                                                                                                                                         Difficile Specific
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Gaps: 0
Identity: 93.333
                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotides
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25794

121

199

seq_documentation_block:

GENERAL INFORMATION:

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seq_documentation_block:
                                      seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-077-939-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-07-849-438-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-528-682-1 x US-07-849-438-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1137
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                                                                              1339 ACTGCTGAAGCAGCTACTGGATGGCAA 1365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1011 TGAAGCAGCTACTGGATGGCAAACT.....ATTGATGGTA 1045
                                                                                                                       155 IleAlaProAlaGluAspGlyTyrArg 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Clo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1948 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               979 GGTAAAAATATTACTTT.....
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 rAspHisAlaArgGlyThrGlnThrGlyPheValArgTyrAspAspGly. 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: WO POFILING DATE: 28-DEC-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                  rgLeuHisArgAsnArgGluTyrArgAspArgTyrTyrArgAsnLeuAsn 154
                                                                                                                                                                                                                                                   AAAAGCAGTTACTGGATGGCAT..
                                                                                                                                                                                                                                                                                                                             AGTAAATTTTTAACTTTGAATGGTAAAAAATATTACTTTGATAATAACTC 1280
                                                                                                                                                                                                                                                                                                                                                                      GlnGluValSerAlaLeuGlyGlyIleProTyr.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eTyrValIleAlaThrAlaProAsnMetPhe......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....AsnValAsnAspValLeuGlyValTyrSerProHisProTyrGlu 110
                                                                                                                                                                                                                                                                                SerGlnIleTyrGlyTrpTyrArgValAsnPheGlyValIleAspGluA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
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44.654
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Percent Identity: 24.528
                                                                                                                                                                  ....AAATATTACTTTAATACTAAC 1338
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O:
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alignment_block:
US-09-528-682-1 x US-08-077-939-16
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; LOCATION:
US-08-077-939-16
                                                                                                                                                                                                       Align seg 1/1 to: US-08-077-939-16
                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/08077939 Patent No. 5521088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 18-JUN-19
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184328/1992
FILING DATE: 18-JUN-1992
                                                                                                                                528 TCAGCTCACATTAGCTTTGAGGGAAAICTGCCTGAAAAATCCAACTCTTT 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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100 ValLeuGlyValTyrSer...ProHisProTyrGluGlnGluValSerAl 115
                                                     578 TACATATTGTTCTACCAACAAGATGGCCAAATCATGAAAATTATTATCGC 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                        84 rIleTyr.ValIleAlaThrAla...ProAsnMetPheAsnValAsnAsp 99
                                                                                                                                                                68 SerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyTyrSerThrTyrTy 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
DEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20007-5109
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3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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YOSHIMOTO, Hiroyuki
MINETOKI, Toshitaka
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18-JUN-1932
                                                                                                                                                                                                                                                                                               78.00
0.743
50.481
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628 AGTTCCGAATACTATTCACGGCCACATCCAGTGCATGATTATATCTCAGT 677

a.....LeuGlyGlyIleProTyrSerGlnIleTyrGlyT 127

ATTACAAGAATTGAAACTGAGTGGTGGTGCTCAATGAACAACCTGAGT

727

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alignment_block:
us-09-528-682-1 x us-08-461-599-16
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US-08-461-599-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE: 18-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 62997/1993
FILING DATE: 26-FEB-1993
PRIOR APPLICATION UNMBER: JP 184328/1992
APPLICATION UNMBER: JP 184328/1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                       187
                                                                                                                                                                   828
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                                                                                                                                                                                                                                                       778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1974 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
928 GATGGTCGGTCTTCGATCCACTTTTTCATGAT...TTAAGAGACGAATT
                                                                                                                                                                                                                                                                                        144 GluTyrArgAspArgTyrTyrArg.....AsnLeuAsnIle.... 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 578 TACATATTGTTCTACCAACAAGATGGCCAAATCATGAAAATTATTATCGC 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                     CysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsnGluGluTh 203
                                                                                                   is...GlnAlaTrpArgGluGluProTrpIleHisHisAlaProGlnGly 186
                                                                                                                                                                                                                                                       TCCTATACTGCAAAAATTTTTAAACTTACTACCACTTTGACTATTCCTTA 827
                                                                                                                                                                                                                                                                                                                                         ACAGTGCAGTAATGAAGCAAATATTAGAAGAATTCAAAAATAGTAAGGGT 777
                                                                                                                                                                                                                                                                                                                                                                                                                         ATTACAAGAATTGAAACTGAGTGGTGTGTGTTCTCAATGAACAACCTGAGT 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a.....LeuGlyGlyIleProTyrSerGlnIleTyrGlyT
                                                                                 ACACAGAAAAGTGGAGAAAATTTATCTTTGTATCTAATCATTGCATGTCT
                                                                                                                                                                 CTTTGGACCAACAGGACCGAGTTGGCGGCTAATTTGTCTTCCAGAAGAGC
                                                                                                                                                                                                         ....AlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProProAspH 171
                                                                                                                                                                                                                                                                                                                                                                            rpTyrArgValAsnPheGlyValIleAspGluArgLeuHisArgAsnArg 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
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346..1923
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50.481
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  974
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seq_documentation_block:

1075

ATAGACTTTAGACCACCGTACTTGTTTATTCCGAAGTCACTTCTTTCGGG 1124

. 231

230

ValAsp.....

1125

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1025

213

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ACAGTGCAGTAATGAAGCAAATATTAGAAGAATTCAAAAATAGTAAGGGT 777

rpTyrArgValAsnPheGlyValIleAspGluArgLeuH1sArgAsnArg 143

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TCCTATACTGCAAAATTTTTTAAACTTACTACCACTTTGACTATTCCTTA 827

156

Sequence 16, Application US/08461599 Patent No. 5658777

APPLICANT:

IWAMATSU, Akihiro YOSHIMOTO, Hiroyuki MINETOKI, Toshitaka BOGAKI, Takayuki

APPLICANT:

FUJII, Toshio

INFORMATION:

APPLICANT: APPLICANT:

NUMBER OF SEQUENCES: 1 APPLICANT: NAGASAWATITLE OF INVENTION:

NAGASAWA, NAOSh1
VENTION: ALCOHOL ACETYLTRANSFERASE GENES
VENTION: THEREOF

AND USE

ADDRESSEE:

STREET: 3000 K Street, CITY: Washington, D.C. COUNTRY: USA ZIP: 20007-5109

3000 K Street, N.W.,

Suite

Foley & Lardner

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,599
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435

Version

#1.25

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-461-599-16

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                            PILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 184328/1992
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/103 K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                          TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                           ID NO:

....CTERISTICS:
1974 base pairs
1YPE: nucleic acid
STRANDEDNESS: don'
TOPOLOGY: 1:
VATURE:
NATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 67
FILING DATE: 26-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
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                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,939
FILING DATE: 18-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NAGASAWA, Naoshi
TITLE OF INVENTION: ALCOHOL ACETYLTRANSFERASE GENES AND USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 05-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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YOSHIMOTO, Hiroyuki
MINETOKI, Toshitaka
BOGAKI, Takayuki
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CDS
346..1923
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seq_name:
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US-09-528-682-1 x US-08-461-621-16
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                                                                                                                   seq_documentation_block:
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                                                                     Sequence 16, Patent No. 5
                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 CysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsnGluGluTh 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          828 CTTTGGACCAACAGGACCGAGTTGGCGGCTAATTTGTCTTCCAGAAGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        678 ATTACAAGAATTGAAACTGAGTGGTGTGTTCTCAATGAACAACCTGAGT
  APPLICANT:
                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 rIleTyr.ValIleAlaThrAla...ProAsnMetPheAsnValAsnAsp 99
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                                                                                                                                                                                                               TTTCATCTACAATCATTTGAGA 1146
                                                                                                                                                                                                                                                                                                                                                                                                   AGGAGGATTACCAATTATTGAGGAAACTTCCAGAACCGATCGAAAAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAATAATATTAAAACTCCACCAAAAAAATTAGATTACATTTTCAAGTACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a....LeuGlyGlyIleProTyrSerGlnIleTyrGlyT
                                                                                                                                                            /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-465-334-16
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                                                                        5, Application US/08465334 5728412
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FUJII, Toshio
IWAMATSU, Akihiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.00
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Percent Identity:
                                                                                                                                                                                                                                                            237
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alignment_scores:
Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-528-682-1 x US-08-465-334-16
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; LOCATION:
US-08-465-334-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: YOSHIMOTO, Hiroyuki
APPLICANT: MINETOKI, Toshitaka
APPLICANT: BOGAKI, Takayuki
APPLICANT: NAGASANA, Naoshi
TITLE OF INVENTION: ALCOHOL ACETYLTRANSFERASE GENES AND USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-465-334-16 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 1974 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 4944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,939
FILING DATE: 18-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 62997/1993
FILING DATE: 26-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: EMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,334
FILING DATE: 05-UN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
628 AGTTCCGAATACTATTCACGGCCACATCCAGTGCATGATTATATCTCAGT 677
                             100 ValLeuGlyValTyrSer...ProHisProTyrGluGlnGluValSerAl 115
                                                                                                                                                                                    528 TCAGCTCACATTAGCTTTGAGGGAAATCTGCCTGAAAAAATCCAACTCTTT 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184328/1992
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                       84 rIleTyr.VallleAlaThrAla...ProAsnMetPheAsnValAsnAsp 99 : ||| |||::: ||| |||||
                                                                                                                                                                                                                             68 SerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyTyrSerThrTyrTy 84
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                                                                                          TACATATTGTTCTACCAACAAGATGGCCAAATCATGAAAATTATTATCGC 627
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Gaps: 10
Percent Identity: 22.115
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	AGENT INFORMATION:
	C-1997
	RENT APPLICATION DATA:
	SYS
	PE: Floppy disk IBM PC compatible
	COMPUTER READABLE FORM:
	COUNTRY: USA
	Wacker Drive, 32nd Floor
	Boehnen Hulbert & Be
	NUMBER OF INVENTION: Genes and Uses
Receptor	No. 6123942el
	APPLICANT: Heffron, Fred
	Hwa, Vivi
	APPLICANT: Sto
	[23942
	<pre>.eq_documentation_block: Sequence 1, Application US/08990470A</pre>
•	eq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-08-990-470A-1
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1124	1075 ATAGACTTTAGACCACCGTACTTGTTTATTCCGAAGTCACTTCTTTCGGG
231	230 ValAsp
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1024	975 AAATAATATTAAAACTCCCACCAAAAAAATTAGATTACATTTTCAAGTACG
213	203 rGlnAsnLeuSerThrIleTyrLeuArgG
974	
203	187 CysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsnGluGluTh
927	878 ACACAGAAAAGTGGAGAAAATTTATCTTTGTATCTAATCATTGCATGTCT
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171	156AlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProProAspH
827	778 TCCTATACTGCAAAATTTTTAAACTTACTACCACTTTGACTATTCCTTA
155	144 GluTyrArgAspArgTyrTyrArgAsnLeuAsnIle
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143	127 rpTyrArgValAsnPheGlyValIleAspGluArgLeuHisArgAsnArg
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127	115 aLeuGlyGlyIleProTyrSerGlnIleTyrGlyT

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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
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; NAME/KEY:
; LOCATION:
; -08-990-470A-1
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US-09-528-682-1 x US-08-990-470A-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-990-470A-1 from: 1 to: 3318
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                                           2065 TCCCAACCTGAAAGCCGAGCGCACGACCACCCACACCCTCTCTGCAAG 2114
                                                                                                                                        2015 TCCGAAGTGTATTTCACTTACAACCACGGTTCGGGTAATTGGCTGCCCAA 2064
                                                                                                                                                                                                                                                                                                                                1942 CTTGGCGGCGCAACTGAATCAGGCTTGGCGTGTCGGCTTACGACATTACTT 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1742 ATCCAGCATCCGGTGAAAACCACCAACTACGGTTTCTCACTGTCTGACCA 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1642 CCGCCTGTCGTTTAAAACTTTCGCCAGCCGCCGTGATTTTGAAAACCTAA 1691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1892 AAAACACCGCCTGCAGCCAACACTTATAAAGGCTGGAGCGGTTTTGTCGG 194:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1792 AATTCAATGGAACGACGTGTTCAGTAGCCGCGCAGGTATCCGTTACGATC 1841
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEPAX: 312-913-0002
                                                                                                                                                                                                                                                                                                                                                                         61 rThrSerLeuSerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuS 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 snLeuTyrAspHis..... 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 tProArgGlyHisAsnGluTyrPheAspArgGlyThrGlnMetAsnIleA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 ArgAlaAspSerArgProProAspGluIleLysArgSerGlyGlyLeuMe 23
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                                                                                                                                                                                                                                                                            erGlyTyrSerThrTyrTyrIleTyrValIleAlaThrAlaProAsn... 93
56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ......ValargTyrasp. 56
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470..2845
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0.601
34.959
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Gaps: 15
Percent Identity: 18.157
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	; MEDLUM TIVE: FIOPDY GISK ; COMPUTER: IBM PC Compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: PatentIn Release #1.0, Version #1.30
	linois USA)6 NDABLE FORM:
	ADDRESSEE: McDonnel STREET: 300 South V
n Receptor	TITLE OF TITLE OF NUMBER O CORRESPO
	APPLICANT: hwd, Ylyiai APPLICANT: Heffron, Fred APPLICANT: Nassif, Xavier
	APPLICANT: Stojiljko APPLICANT: So, Magda ADDITCANT: Hwa Vivi
	<pre>seq_documentation_block: Sequence 1, Application US/08817707 Patent No. 6277382 GENERAL INFORMATION:</pre>
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2365	4 CAAAGTAGCGTCTTTGTTCC
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ت ن	::
139	123 lnIleTyrGlyTrpTyrArqValAsnPheGlyVa
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	seq_documentation_block: seq_documentation_block: patent No. 6087559 GENERAL INFORMATION: APPLICANT: Nichols, Scott E. APPLICANT: Nichols, Scott E. TITLE OF INVENTION: Latexes in Paper Manufacture FILLE REFERENCE: 0356D CURRENT APPLICATION NUMBER: US/09/007,999 CURRENT FILING DATE: 1998-01-16 EARLIER APPLICATION NUMBER: 08/478,704 EARLIER FILING DATE: 1995-06-07 NUMBER OF SEQ ID NOS: 2 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO I SEQ ID NO I LENGTH: 4460 TYPE: DNA
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222 2548	217
216 2498	206 uSerThrIleTyrLeuArgGluTyrGlnSer
206 2448	190 SerSerArgThrIleThrGlyAspThrCysAsnGluGluThrGlnAsnLe
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123 2264	120ProTyrSerG
119 2214	109TyrGluGlnGluValSerAlaLeuGlyGlyIle
2164	2115 GCCGCAGCGAAAAAGGTACTTTGGATGCCAACCTGTATCAAAGCAATTAC
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108 2114	107 spro
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US-09-007-999-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 euArgSerAlaHisLeuAlaGlyGlnSerIleLeuSer...GlyTyrSer 81
|||:::::: ||| :::::::::|| |||
3246 ..ACGAGTGGTTACCAAGCCAAAAATACTTTCATCAGCGAAGGTGATAAA 3293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3121
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                                                                                                     3614 ATATTTGATAAGCAATCTGGGAACATGTACCGTAATCGTTTATTGAAA 3663
                                                                                                                                                                                                                                                                                                                              3514 GTGTTGGATTAACTGTAATTGATGGTCAGGTTCAATACTTTGATGAAATG 3563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3394 CTATTCTTAAGAATGAAGATGGAACTTACGCTTATTATGGAAATGACGGT 3443
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                                               152 snLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPhePro 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 tPheAsnValAsn.....AspV 100
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                                                                                                                                                                                                                   GGCTATCAAGCCAAAGGAAAATTTGTAACAACTGCCGATGGTAAAATAAG 3613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGly..... 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nThrGlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rGlyGlyLeuMetProArgGlyHis.AsnGluTyrPheAspArgGlyThr 35
                                                                                                                                                                                                                                                                                                                                                                                                                                      .....TGGCGTCACTTCAATAATGGTGAAATGA 3513
                                                                                                                                                                                                                                                                                                                                                                                .................ValIleAspGluArgLeuHisArgAsnArgGlu... 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .........ProHisProTyrGluGlnGluValSerAlaLeuGlyGlyIl 119
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Ratio:
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Gaps: 16
Percent Identity: 20.333
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3665
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; NAME/KEY: CDS
; LOCATION: (9)...(4434)
US-09-210-361-1
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Quality:
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CURRENT FILING DATE: 1998-12-11
EARLIER APPLICATION NUMBER: 09/007,999
EARLIER FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/478,704
EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1998-01-20
EARLIER APPLICATION NUMBER: 09/009,620
EARLIER APPLICATION NUMBER: 08/485,243
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EARLIER APPLICATION NUMBER: 09/008,172
EARLIER APPLICATION NUMBER: 08/482,711
EARLIER FILING DATE: 1998-01-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-210-361-1
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 1
LENGTH: 4460
TYPE: DNA
ORGANISM: streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09210361 Patent No. 6284479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Substitutes for modified Starches
TITLE OF INVENTION: Latexes in Paper Manufacture
FILE REFERENCE: 0357CR
                                                                                                                  3121 A.....
                                                                                                                                                                                                                               3077 GACAAATATTTTAGGGCGCGGGGCAGGCTATGT.....CTTAAAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3721 AAACCATTAACGGTCAACACCTGTACTTTAGAGCAAACGGTGTTCAGGTC 3770
3153 AATAAAGAAATAAACTTCCTTCCTAAAACATTGTTAAACCAAGATAGTCA 3202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 LysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyrAsn 234
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0.610
42.333
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20.333
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                                       GENERAL INFORMATION: Bruce W
APPLICANT: Chesebro, Bruce W
APPLICANT: Caughey, Byron W
APPLICANT: Chabry, Joelle
APPLICANT: Priola, Susette
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ....CTCGGTGAAGATGGTGCAGCAGTGACAGGA......TCTC 3720
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                                                                                                                                                                                                                                                                                                                                                                                                ANACCATTAACGGTCAACACCTGTACTTTAGAGCAAACGGTGTTCAGGTC 3770
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Inhibitors
  Protein
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                      of Formation
                      of Protease
                      Resistant
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PREADLES: DNA
DROANTES: MUS musculus
FEATURES: CDS
NAME/KEY: CDS
LOCATION: (101)..(865)
US-09-128-450-27
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; Sequence 27, Application US/09823494
; Patent No. 6355610
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US-09-528-682-1 x US-09-128-450-27
APPLICANT: Chesebro, Bruce W
APPLICANT: Caughey, Byron W
APPLICANT: Chabry Joelle
APPLICANT: Priola, Susette
TITLE OF INVENTION: Inhibitors of Formation
TITLE OF INVENTION: Protein
FILE REFERENCE: 50121
CURRENT APPLICATION NUMBER: US/09/823,494
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/128,450
                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-823-494-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-09-128-450-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
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CURRENT APPLICATION NUMBER: US/09/128,450
CURRENT FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1322
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PRIOR FILING DATE: 1998-08-03 NUMBER OF SEQ ID NOS: 29

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(865)
US-09-823-494-27
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                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-326-670A-1
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SEQ ID NO 27
LENCTH: 1322
TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                 Sequence 1, Application US/08326670A Patent No. 5698438
                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                   APPLICANT: Nassif, Xavier
TITLE OF INVENTION: A No. 5698438el Bacterial Hemoglobin Receptor Gene and Uses
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                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                    NUMBER OF SEQUENCES:
                                      STREET:
                                                           ADDRESSEE:
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                                                                                                                                                           So, Magdalene
Hwa, Vivian
Heffron, Fred
Illinois
                                    E: Allegretti & Witcoff, Ltd.
10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                       Stojiljkovic,
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1.149
54.032
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Gaps: 6
Percent Identity: 24.194
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alignment_block: us-09-528-682-1 \times us-08-326-670A-1
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; LOCATION:
US-08-326-670A-1
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FILING DATE: 18 OCT 1994
CLASSIFICATION: 536
ATTORNEY_AGENT INFORMATION:
NAME: NO. 5698438nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 94,784
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TETEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 810-221-8317
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                        1792 AATTCAATGGAACGACGTGTTCAGTAGCCGCGCAGGTATCCGTTACGATC 1841
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                                                 1892 AAAACACCGCCTGCAGCCAACACTTATAAAGGCTGGAGCGGTTTTGTCGG
                                                                                                                                            1842 ATACCAAAATGACGCCTCAGGAATTGAATGCCGAGTGTCATGCTTGTGAC 1891
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 3318 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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61 rThrSerLeuSerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuS 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 tProArgGlyHisAsnGluTyrPheAspArgGlyThrGlnMetAsnIleA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 ArgAlaAspSerArgProProAspGluIleLysArgSerGlyGlyLeuMe 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                 .....AlaArgGlyThrGlnThrGlyPhe...............
                                                                                                                                                                                                                                                                               .....ValArgTyrAsp. 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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0.593
34.959
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Percent Identity:
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                                                                                      .....AspGlyTyrValSe 61
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15
18.157
                                                 1941
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1942 CTTGGCGGCGAACTGAATCAGGCTTGGCGTGTCGGTTACGACATTACTT 1991

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seq_documentation_block:
; Sequence 47, Application US/08482918
; Patent No. 6207417
                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-482-918-47
                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2065 TCCCAACCTGAAAGCCGAGCGCACGACCACCCACACCCTCTCTGCAAG 2114
                                                                                                                                                                                                                                                                                                                                                                                              2599 AAAAGAT 2605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2549 TACACCGTTTATGAAAACAAGGGCTGGGGTACGCCTTTGCAGAAAAAGGT 2598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2499 TGTTCTCCCGCCTGACCTATCTGGGCGCGAAAAAGGTCAAAGACGCGCAA 2548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2449 GAAAGTGATTGCCGGTATCGACTATGAAAGTCCGAGCGAAAAATGGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2405 AGCAAA.....CTGTCGGGCGACAACAGCCTGCTGTCCACCCAGCCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2265 AAAAACTGGAATGGCAGATGCAAAAT.....ATCGACAAGGCCAGA 2305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2215 CTGTACTCAGATGAATTACTACTACGGTATGTGTAGCAATCCTTATTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2165 CGCAATTTCCTGTCTGAAGAGCAGAAGCTGACCACCAGCGGCGATGTCAG 2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2115 GCCGCAGCGAAAAAGGTACTTTGGATGCCAACCTGTATCAAAGCAATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2015 TCCGAAGTGTATTTCACTTACAACCACGGTTCGGGTAATTGGCTGCCCAA 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 SerSerArgThrIleThrGlyAspThrCysAsnGluGluThrGlnAsnLe 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 laTrpArgGluGluProTrpIleHisHisAlaProGlnGlyCysGlyAsn 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 aProAlaGluAspGlyTyrArgLeuAlaGlyPheProProAspHisGlnA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 HisArgAsnArgGluTyrArgAspArgTyrTyrArgAsnLeuAsnIleAl 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108
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                   APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
APPLICANT: Martin, Francis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 eArgAsp 238
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 erGlyTyrSerThrTyrTyrIleTyrValIleAlaThrAlaProAsn...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCCGCGGTATCGAGCTGACGGGCCGT.....CTGAATGTGGA 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PheSerAspTyrGlnSerGlu.....ValAspIleTyrAsnArgIl 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lnIleTyrGlyTrpTyrArgValAsnPheGlyValIleAspGluArgLeu 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....MetPheAsnValAsnAspValLeuGlyValTyrSerProHi 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....ProTyrSerG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....LysValLysArgGlnIle 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....GAGGGCTGGAAACTGTTCGGCTCGCTGGGTTATGCGAAA 2404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....TyrGluGlnGluValSerAlaLeuGlyGlyIle.. 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ......AAAGTAGCGTCTTTTGTTCCT....... 2365
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alignment_block:
US-09-528-682-1 x US-08-482-918-47
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US-08-482-918-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 0101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEFX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                    362 TCAGCAGCCGGCTTCGCTCGC...........CGCCTCGCGCCGAGACT
                                                                                                                                              341
                                                                                                                                                                                                                                                                                         245 CGCCCTCCCGATTCTTCCCTCCGCGCCCTTGCCTGCTTCTCGCCTACCCC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 5864 base pairs
400 AGAAGCGCTGCGGGAAGCAGGGACAGTGGAGAGGGGCGCTGCGCTCGGGCT
                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
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                   64 u...SerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyT
                                                                                         48 ThrGlnThrGlyPheValArgTyrAspAspGlyTyrValSerThrSerLe ::: :::::: ||
                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                            31 heAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGly 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6300 :
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                     .....GlyGlyLeuMetProArgGlyHisAsnGluTyrP
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Ratio:
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3932..4088, 431
5677..5713)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
join(1744..1797, 2693..2755, 3351..3521, 3932
..4088, 4314..4397, 4778..4887, 5208..5275, 5677
..5713)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.50
0.850
42.056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 214
Gaps: 12
Percent Identity: 25.234
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                                                                                                                                            ....CTGTATAAAAGCGCCGGCGGC
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                                                                      399
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PRIOR APPLICATION DATA:

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-224-681-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for
TITLE OF INVENTION: Transfer wi
                                          PRIOR APPLICATION DATA:
                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149
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                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                                                                                                                        APPLICATION NUMBER: 09/0 FILING DATE: 12-JAN-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300
CITY: Chicago
APPLICATION NUMBER: 07/9
                                                             CLASSIFICATION:
                                                                                 APPLICATION NUMBER: FILING DATE: 24-MA
                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Illinois COUNTRY: United
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isAlaProGlnGlyCysGlyAsnSerSerArgThrIle
    :::|||||||||::::: |||    :::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aGlyPheProProAspHisGlnAlaTrpArgGluGluProTrpIleHisH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TyrTyrArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAl 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAGGGCGCCCCGGGAGCTCCCCAGGCTC......612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuGlyGlyIleProTyrSerGln.IleTyrGlyTrpTyrArgValAsnP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGTGCTGGATCGCACCGCTGCCTTTCCTTATGAAGAAGACACAAGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCCAATGCGTGGACTATCTGCCGCCGCTGTTCGTGCAATATGCTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGAGACAAGAGGATGCGGGGGGGGGGCGGGGTGGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heGlyValIleAspGluArgLeuHisArgAsnArgGluTyrArgAspArg 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ......HisProTyrGluGlnGluValSerAla 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yr.....SerThrTyrTyrIleTyrValIle.AlaThrAl 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47,
                                                                                                                                                                                                                                                                                                                                                                                                     60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /, Application US/09224681 6207454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Marshall, O'Toole, 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                     United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zsebo, Krisztina M.
                                                                               24 -MAY -1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Method for Enhancing the Efficiency of Gene Transfer with Stem Cell Factor (SCF) Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104
                      07/982,255
                                                                                                                                                                               09/005,893
                                                                                                                                                                                                                                                            US/09/224,681
                                                                                                   08/449,653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerstein, Murray & Borun
South Wacker Drive
                                                                                                                                                                                                                                                                                                 Version #1.30
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alignment_block:
us-09-528-682-1 x us-09-224-681-47
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    Quality:
    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-224-681-47
                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-09-224-681-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5864 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Clough, David W.
REGISTACION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
                                                                     400
                                                                                                                                          362
                                                                                                                                                                                                             341
                                                                                                                                                                                                                                                                                   295
                                                                                                                                                                                                                                                                                                                                                      245 CGCCCTCCCGATTCTTCCCTCCGCGCCCTTGCCTGCTTCTCGCCTACCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 01-OCT-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                      64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/5: FILING DATE: 11-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                          ThrGlnThrGlyPheValArgTyrAspAspGlyTyrValSerThrSerLe ::: :::|||||| :::::: |||
ACCCAATGCGTGGACTATCTGCCGCCGCTGTTCGTGCAATATGCTGGAGC
                                                                     AGAAGCGCTGCGGGAAGCAGGGACAGTGGAGAGGGCGCTGCGCTCGGGCT
                                                                                                    u...SerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyT
                                                                                                                                          TCAGCAGCCGGCTTCGCTCGC...........CGCCTCGCGCCGAGACT
                                                                                                                                                                                                                                              heAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGly
                                                                                                                                                                                                                                                                               yr.....SerThrTyrTyrIleTyrValIle.AlaThrAl 91
                                                                                                                                                                                                                                                                                                                  .....GlyGlyLeuMetProArgGlyHisAsnGluTyrP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
join(1744..1797, 2693..2755, 3351..3521, 3932
...4088, 4314..4397, 4778..4887, 5208..5275, 5677
...5713)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(565..579, 1684..1797, 2693..2755, 3351..3521, 3932..4088, 4314..4397, 4778..4887, 5208..5275, 5677..5713)
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0.850
42.056
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107 500

19

aProAsnMetPheAsnValAsnAspValLeuGlyValTyrSerPro.... 106

535 TTGTGCTGGATCGCACCGCTGCCTTTCCTTATGAAGAAGACACAAGTGAG 584

TCCAGAACAGCTAAAC............GGAGTCGCCACACCACTGT 534

LeuGlyGlyIleProTyrSerGln.IleTyrGlyTrpTyrArgValAsnP 132

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alignment_block:
US-09-528-682-1 x US-08-336-728A-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                             341
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                     107
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                                                                                                                                                                                                                                                                                                                                                                  362 TCAGCAGCCGGCTTCGCTCGC......CGCCTCGCGCGCGAGACT 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 heAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGly 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 .....GlyGlyLeuMetProArgGlyHisAsnGluTyrP 31
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LOCATION:
LOCATION:
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Clough, David W. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 5864 base pairs
TAGGGCGCGCCCGGGAGCTCCCAGGCTC
                                                                                                                                                                            aProAsnMetPheAsnValAsnAspValLeuGlyValTyrSerPro.... 106
                                                                                                                                                                                                                                                                                             AGAAGCGCTGCGGGAAGCAGGGACAGTGGAGAGGGGCGCTGCGCTCGGGCT 449
                                                                                                                                                                                                                  ACCCAATGCGTGGACTATCTGCCGCCGCTGTTCGTGCAATATGCTGGAGC 499
                                                                                                                                           TCCAGAACAGCTAAAC....
                                                                      TTGTGCTGGATCGCACCGCTGCCTTTCCTTATGAAGAAGACACAAGTGAG
                                                                                                       ......HisProTyrGluGlnGluValSerAla 115
                                                                                                                                                                                                                                             yr.....SerThrTyrTyrIleTyrVallle.AlaThrAl 91
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join(1744..1797, 2693..2755, 3351..3521, 3932
..4088, 4314..4397, 4778..4887, 5208..5275, 5677
..5713)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(565..579, 1684..1797, 2693..2755, 3351..3521,
3932..4088, 4314..4397, 4778..4887, 5208..5275,
5677..5713)
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0.850
42.056
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                                                                                                                                             .....GGAGTCGCCACACCACTGT 534
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seq_documentation_block:

182 648 165

aGlyPheProProAspHisGlnAlaTrpArgGluGluProTrpIleHisH 182

TyrTyrArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAl 165

.....TCCAGGAAAAATCGCGCCCCGG 633 heGlyValIleAspGluArgLeuHisArgAsnArgGluTyrArgAspArg 148

149 613 132

Patent No. Sequence 47,

/, Application US/08336728A 6207802

GENERAL INFORMATION:

APPLICANT:

Zsebo, Krisztina M.

APPLICANT:
APPLICANT:

APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor

CORRESPONDENCE ADDRESS:

ADDRESSEE:

E: Marshall, O'Toole, 6300 Sears Tower, 233

Gerstein, Murray & South Wacker Drive

& Borun

Chicago

Illinois

NUMBER OF SEQUENCES:

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-336-728A-47

GTGAGACAAGAGGATGCGGGGGGGGGGGCGGGGGTGTG 735 isAlaProGlnGlyCysGlyAsnSerSerArgThrIle 194

FILING LALL.

CLASSIFICATION: 424

PRIOR APPLICATION NUMBER: 07/982,255

EILING DATE: 25-NOV-1992

PRIOR APPLICATION NUMBER: 07/589,701

EILING DATE: 01-OCT-1990

PRIOR APPLICATION NUMBER: 07/573,616

FILING DATE: 24-AUG-1990

PRIOR APPLICATION NUMBER: 07/573,616

FILING DATE: 24-AUG-1990

PRIOR APPLICATION NUMBER: 07/573,198

PRIOR APPLICATION NUMBER: 07/537,198

FILING DATE: 11-JUN-1990

PRIOR APPLICATION NUMBER: 07/537,198

FILING DATE: 11-JUN-1990

ATTORNEY/AGENT INFORMATION

APPLICATION NUMBER:

MBER: 07/422,383 16-OCT-1989

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

COUNTRY:

United States of

America

60606-6402

SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

US/08/336,728A

APPLICATION NUMBER: US/0 FILING DATE: 09-NOV-1994

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alignment_scores:
Quality:
Ratio:
alignment_block:
US-09-528-682-1 x US-08-537-361E-5
                                                                                                                                                                                                      ; NAME/KEY:
; LOCATION:
US-08-537-361E-5
                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: NO. 6121037nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 94,784-A
TELECOMMUNICATION INFORMATION:
TELEFAX: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2379 base pairs
TYPE: nucleic acid
cmpa.Numpraners: sindle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-537-361E-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5,
Patent No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/537,361E
FILING DATE: 02-0CT-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Stojiljkovic, Igor
APPLICANT: So, Magdalene
APPLICANT: Hwa, Vivian
APPLICANT: Heffron, Fred
APPLICANT: Heffron, Fred
APPLICANT: Nassif, Xavier
TITLE OF INVENTION: No. 6121037el Bacterial Hemoglobin Receptor
TITLE OF INVENTION: Genes and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 aGlyPheProProAspHisGlnAlaTrpArgGluGluProTrpIleHisH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 TyrTyrArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAl 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 isAlaProGlnGlyCysGlyAsnSerSerArgThrIle 194
                                                                                                                                                                                                                                                                                       STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  698 GTGAGACAAGAGGATGCGGGGGGAGGCCGGCGTGGTGTG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 60606
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36.644
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Gaps: 13
Percent Identity: 19.521
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230 alAspIleTyrAsnArgIleArgAsp 23 :: ::: ::::::::::	217 .LysVallysArgGlnIlePheSerAspTy 2061 AAAGGTCAAAGACGCGCAATACACCGTTTA	216	200 snGluGluThrGlnAsnLeuSerThrIleT 	183 aProGlnGlyCysGlyAsnSerSerArgT : ::::: ::: 1917 CTCGCTGGGTTATGCGAAAAGCAAA	167 PheProProAspHisGlnAlaTrpArgGluG 1888 TTTGTTCCT	150 yrargasnLéuasnIlealaProAlaGlu :: 1864CTGAATGTGGAC	133 yVallleAspGluArgLeuHisArgAsnA ::: 1822ATCGACAAGGCCAGAATCCGCGGTP	120ProTyrSerGlnIleTyrGl ::: 1777 TGTAGCAATCCTTATTCCGAAAAACTGGA	114 eralaLeuGlyGlyIle	109	CTCTCTCTGCAAGGCCGCAG	108	101 euGlyValTyrSerProHisPro ::: ::: 1577 CGGGTAATTGGCTGCCCAATCCCAACCTG	88 eAlaThrAlaProAsnMetPhe ::::	72 AlaGlyGlnSerIleLeuSerGlyTyrSe:::	55 yraspaspGlyTyrValSerThrSerLeuSerLeuArgSerAlaHisLe ::: ::: ::: ::: ::: 1459AGCGGTTTTGTCGGCTTGGCGGCGCAACTGAATCAGGCTTGGCG	45AlaArgGlyThrGlnThrGlyPhe	42 Tyrasphis	Align seg 1/1 to: US-08-537-361E-5
38	PyrGlnSerGlu	CCTGACCTATCTGGGCGCGAA 2060	TyrLeuArgGluTyrGlnSer 216 	hrIleThrGlyAspThrCysA 200 :::::: :::CTGTCGGGCGACAACAGCC 1960	luGluProTrpIleHisHisAl 183 :: GAGGGCTGGAAACTGTTCGG 1916	:luAspGlyTyrArgLeuAlaGly 166 ::::: :::AAAGTAGCGTCT 1887	gAsnArgGluTyrArgAspArgTyrT 150 ::: сдтатсдадстдасдддсссст 1863	GlyTrpTyrArgValAsnPheGl 133 GAATGGCAGATGCAAAAT 1821	ATGAATTACTACTACGGTATG 1776	TyrGluGlnGluValS 114	GTACTTTGGA			MetPheAsnValAsnAspValL 101 ::: TATTTCACTTACAACCACGGTT 1576	erThrTyrTyrIleTyrValIl 88	SerLeuArgSerAlaHisLeu 71 ::: ::::: GAACTGAATCAGGCTTGGCGT 1503	PhrGlnThrGlyPheValArgT 55	AGGAATTGAATGCCGAGTGTCATGC 1415	from: 1 to: 2379

2111 CGCCTTTGCAGAAAAAGGTAAAAGAT 2136

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alignment_block:
US-09-528-682-1 x US-08-210-535-5
                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: US-08-210-535-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                 Align seg 1/1 to: US-08-210-535-5 from: 1 to: 4899
                                                                                                                                                                                                                                                                                                                     Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/820,701
FILING DATE: 10-Jan-1992
APPLICATION NUMBER: DE 41 00 704.2
FILING DATE: 11-Jan-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 41 40 699.0
FILING DATE: 10-Dec-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5965424man D.
REGISTRATION NUMBER: 30,946
BEFERENCE (FOCKET NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: HU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 88-3884
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     equence 5, Applicati
atent No. 5965424
GENERAL INFORMATION:
                                          1595 AACCTATATTTCGGTTTCCGTGGCGGTCGTTTGGATGCCAATGGCAATGA 1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 803
CITY: New York
STATE: New York
STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PS C COMPUTER: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/210,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ambrosius, Dorothea
APPLICANT: Dony, Carola
APPLICANT: Rudolph, Rainer
TITLE OF INVENTION: Recombinant IgA Protease
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                41 ....LeuTyrAspHisAlaArgGlyThrGlnThrGly.....PheValA 54
54 rgTyrAspAspGlyTyrValSerThrSerLeuSerLeuArgSerAlaHis 70
                                                                                                                                                       28 AsnGluTyrPheAsp...ArgGlyThrGlnMetAsnIleAsn...... 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4899 base pairs
                                                                                                                                                                                                                                                                                                                     76.00
1.056
45.000
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Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                   160
6
20.625
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; NAME/KEY:
; LOCATION:
US-08-408-095-26
                                                              alignment_scores:
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                                                                                                                                                                                                                                                                        TELEPAX: (202) - 26
INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
1.FNGTH: 946 base pairs
  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26, Application US/08408095 Patent No. 5858678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1922 AACGGTGTAGCAGAAAATAACGACTGGATC: 1951
                                                                                                                                                                                                                                                                                                                                                   NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
TELECOMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEPAX: (202)293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chinnadurai, Govindaswamy TITLE OF INVENTION: APOPTOPSIS-REGUL NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 HisGlnAlaTrpArgGluGluProTrpIle 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                   TOPOLOGY: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/01
FILING DATE: 21-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGATGAAGATGATTATAGTTATTACCGACCAAGGCGACCCATCCCA 1840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yrSerProHisProTyrGluGlnGluValSerAlaLeuGlyGlyIlePro 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTATTACGCCCTAAAATCCGGCGGCAGGCTGAACGCACCGATGCCCGAG 1921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyrArgAsnLeuA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyValIleAspGl 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 snIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProProAsp 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ....ACCAATCCGAACAGCCTTTCGGTACATAGCATACAAAATGACT 1790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lileAlaThrAlaProAsnMetPheAsnValAsnAspValLeuGlyValT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-408-095-26
                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington : D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20037
                     Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                             CDS
26..505
                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                              CDNA
75.00
1.119
41.615
                                                                                                                                                                                                                                                     single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/408,095
                                                                                                                                                                                                                                                                                                                                        26:
  Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
                                        Length:
                     Gaps:
    21,118
                                        161
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alignment_block:
US-09-528-682-1 x US-08-408-095-26/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
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US-09-182-117-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: US-08-408-095-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application Patent No. 6204436
                                                                                                                                                                      CLASSIFICATION:
INFORMATION FOR SEQ ID NO:
.SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                              TITLE OF INVENTION: Transgenic Plant
NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/182,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175
                  HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 441 GCCAGCAGCACCTGTTCGCAGGACACCCAGGAC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 691
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                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                541 GTGGGGCCAGCCACGCCCTGAGCCGGGGCCTCACTTGAGCAGCAGGT 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       741 CGGTGACAATTGCAGAGCCATAGGAATTCATCTTTTAGAAAAAAACGAAAA 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          782 CAGGAGTGAATGGCTCT.....TCCTGGGCACAGGCCACAGTTAAC 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 lyGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGly 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     832 CACAGGGGTGTGACCAGCACTCCCCCTGCTACCTGCCGTGTGGGCAGGGG 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             882 CTCCTCGGAATCTATTCCAGTAGATTCTTTGCCGAGGGCATCACATATCA 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                        STRANDEDNESS:
                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                              FILING DATE:
                                                                                       TOPOLOGY:
                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrGlyAspThrCysAsnGluGluThrGlnAsn 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ys......GlyAsnSerSerArgThrIle 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAAAAAGATAACAGCAGCAGGCCGCCACCTCCAGGGCAGTGGTCATGGGG 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGCACTATCTCGGGGTTTAAATATAAAAAGGCATCATGAGAAAACAGT 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lyTyrArgLeuAlaGlyPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGAATAAAAAAAAAACAAAAAACCTGAGTATAAAACCTCAGCAGTGTT 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ......AspArgTyrTyrArgAsnLeuAsnIleAlaProAlaGluAspG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....ProTyrGluGlnGluValSerAlaLeuG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....ProProAspHisGlnAlaTrp.. 174
                                                                                                                                                 8012 base pairs
                    ĕ
                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ....ArgGluGluProTrpIleHisHisAlaProGlnGlyC 187
                                         NO
                                                              DNA (genomic)
                                                                                                          double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/0918211
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- O/ptodata/2/pna/US090_CUMB.seq:US-60-245-222-80 - 88.
2_6/ptodata/2/pna/US6024_COMB.seq:US-60-245-222-80 - 88.
2_6/ptodata/2/pna/US99B_COMB.seq:US-09-948-941-555 - 88.
2_6/ptodata/2/pna/US99B_COMB.seq:US-60-226-176-834 - 88.
12_6/ptodata/2/pna/US6022_COMB.seq:US-60-233-468-834 - 88.
12_6/ptodata/2/pna/US6023_COMB.seq:US-60-313-371-834 - 88.
12_6/ptodata/2/pna/US6017_COMB.seq:US-60-313-371-834 - 88.
12_6/ptodata/2/pna/US6017_COMB.seq:US-60-173-464-15217 + 10-6/ptodata/2/pna/US6017_COMB.seq:US-60-173-464-15217 + 10-6/ptodata/2/pna/US6016_COMB.seq:US-60-173-464-15217 + 10-6/ptodata/2/pna/US6016_COMB.seq:US-60-173-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /US6016_COMB.seq:US-60-167-217-18;
/US098A_COMB.seq:US-09-803-736-14
/US098A_COMB.seq:US-09-221-222B-85
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/US093_COMB.seq:US-09-365-530-1 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMB
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$6.00 $99.20 $4.5e+.

$6.50 $159.44 $17.

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$6.50 $159.43 $67.

$6.50 $149.83 $67.

$6.50 $149.83 $2.

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$6.50 $144.60 $1.

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_6/ptodata/2/pna/US6054_COMB. seq. u
_6/ptodata/2/pna/US095B_COMB. seq. u
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_6/ptodata/2/pna/US095B_COMB. seq. u
                                                                                                                         /ptodata/2/pna/PCTUS_COMB.seq.PCT-US99-30747-8
/ptodata/2/pna/PCTUS_COMB.seq.PCT-US99-30747-17
/ptodata/2/pna/PCTUS_COMB.seq.PCT-US99-30747-19
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/ptodata/2/pna/US094_COMB.seq.US-09-470-124-17
/ptodata/2/pna/US094_COMB.seq.US-09-470-124-17
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Cygn2_6/ptodata//ppa//S099B_COMB. seq:US-09-175-972-991-10184-75.
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Cygn2_6/ptodata//ppa//S099A_COMB. seq:US-09-252-991A-1644-75.
Cygn2_6/ptodata//ppa//S099A_COMB. seq:US-09-252-991A-1631-75.
Cygn2_6/ptodata//ppa//S099A_COMB. seq:US-09-252-991A-1634-75.
Cygn2_6/ptodata//ppa//S099A_COMB. seq:US-09-252-991A-10045-75.
Cygn2_6/ptodata//ppa//S099A_COMB. seq:US-09-252-991A-10045-75.
Cygn2_6/ptodata//ppa//S099A_COMB. seq:US-09-252-991A-10045-75.
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Cygn2_6/ptodata//ppa//S099A_COMB. seq:US-09-252-991A-10045-75.
Cygn2_6/ptodata//ppa//S099A_COMB. seq:US-09-252-991A-10045-75.
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                                                                      7C_COMB. seq: US-09-76
0. COMB. seq: US-10-092
0. COMB. seq: US-60-20
20. COMB. seq: US-60-20
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__COMB.seq:US-09-189
C_COMB.seq:US-09-86
O_COMB.seq:US-60-20
5_COMB.seq:US-60-25
5_COMB.seq:US-09-94
B_COMB.seq:US-09-94
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/cgn2_6/ptodata/2/pna/US6020_COMB.seq:US-60-205-419-111 + /cgn2_6/ptodata/2/pna/US6020_COMB.seq:US-60-205-419-112 + /cgn2_6/ptodata/2/pna/US6020_COMB.seq:US-60-205-419-113 + /cgn2_6/ptodata/2/pna/US6020_COMB.seq:US-60-205-419-113 + /cgn2_6/ptodata/2/pna/US6020_COMB.seq:US-60-205-419-114 + /cgn2_6/ptodata/2/pna/US6020_COMB.seq:US-60-205-419-116 + /cgn2_6/ptodata/2/pna/US6020_COMB.seq:US-60-205-419-116 + /cgn2_6/ptodata/2/pna/US6020_COMB.seq:US-60-205-419-117 + /cgn2_6/ptodata/2/pna/US6020_COMB.seq:US-60-205-419-119 + /cgn2_6/ptodata/2/pna/US6020_COMB.seq:US-60-205-419-119 + /cgn2_6/ptodata/2/pna/US6020_COMB.seq:US-60-205-419-120 + /cgn2_6/ptodata/2/pna/US6020_COMB.seq:US-60-205-419-121 + /cgn2_6/ptodata/
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TYPE: DNA
; ORGANISM: Plasmid PPJV2004
US-09-724-315-4
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CURRENT FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: ARRINGTON, JOSHUA
TITLE OF INVENTION: NUCLEIC ACID ADJUVANTS
FILE REFERENCE: APF41
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; ORGANISM: Escherichia coli
US-09-950-335A-5
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US-09-528-682-1 x US-09-950-335A-5
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SEQUENCE 5, APPLICATION US/09950335A

GENERAL INFORMATION:
APPLICANT: HONE, DAVID M.

TITLE OF INVENTION: GENETICALLY ENGINEERED CO-EXPRESSION DNA VACCINES, CONSTRUCTION TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 4115-128

CURRENT APPLICATION NUMBER: US/09/950,335A

CURRENT FILING DATE: 2001-09-10

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin version 3.1

SEQ ID NO 5

LENGTH: 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-09-950-335A-5
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Ratio: 5.410
milarity: 99.583
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seq_documentation_block:
    Sequence 3, Application PC/TUS9930747
    GENERAL INFORMATION:
    APPLICANT: Boyce Thompson Institute for Plant Research at Cor
    TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Exp:
    TITLE OF INVENTION: Transgenic Plants
    FILE REFERENCE: 4868/85427
    CURRENT APPLICATION NUMBER: PCT/US99/30747
    CURRENT FILING DATE: 1999-12-22
    NUMBER OF SEQ ID NOS: 67
    SOFTWARE: Patentin Ver. 2.1
    SEQ ID NO 3
    LENGTH: 782
OTHER INFORMATION: Description of Artificial Sequence:E., OTHER INFORMATION: heat-labile toxin gene mutagenized to OTHER INFORMATION: expression in plants.

PCT-US99-30747-3
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                                                    FEATURE:
NAME/KEY: CDS
LOCATION: (3)..(782)
FEATURE:
                                                                                                    TYPE: DNA
ORGANISM: Artificial
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                                              GAGGAGACCCAAAACCTTAGCACCATCTACCTTAGGAAGTACCAATCCAA
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Ratio: 5.362
Similarity: 100.000
            snArgIleArgAspGluLeu
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                                                                                                                                           CACAAGGTTGTGGAGACTCCTCAAGGACCATCACAGGTGACACTTGCAAT
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seq_documentation_block:

seq_name:

/cgn2_6/ptodata/2/pna/US094_COMB.seq:US-09-470-124-3

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; OTHER INFORMATION: Description of Artificial Sequence:E.; OTHER INFORMATION: heat-labile toxin gene mutagenized to; OTHER INFORMATION: expression in plants.
US-09-470-124-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-528-682-1 x US-09-470-124-3
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Ratio: 5.362
Percent Similarity: 100.000
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APPLICANT: Arntzen
APPLICANT: Arntzen
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/84454
CURRENT APPLICATION UMBER: US/09/470,124
CURRENT FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
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LENGTH: 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                           134 allleAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyr 150
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ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh
                                                                                                                                                         yGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyV 134
                                                                                                                                                                                                                                                                                                                                                                                                   gSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyTyrSerThrTyrT
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                                                         TGATTGATGAGGGCTCCATAGGAATAGGGAGTATAGGGACAGGTACTAT
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98.333
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; LENGTH: 5488
; TYPE: DNA
; ORGANISM: plasmid pPJV2007
US-09-724-315-6
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; Sequence 6, Application US/09724315
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-528-682-1 x US-09-724-315-6
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HAYNES, JOE1 R.
APPLICANT: ARRINGTON, JOSHUA
TITLE OF INVENTION: NUCLEIC ACID ADJUVANTS
FILE REFERENCE: APF41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/724,315
CURRENT FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 22
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99.576
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Percent Identity:
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seq_documentation_block:
; Sequence 5, Applicatio
; GENERAL INFORMATION:
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                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Domenighini, Mario
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
TITLE OF INVENTION: Immunogenic Detoxified Mutants of
TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation
TITLE OF INVENTION: Their Use for the Preparation of Vaccines
NUMBER OF SEQUENCES: 41
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                   NAME: McClung, Barbara G.
REGISTARTION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0315.001
TELECOMMUNICATION INFORMATION:
                                                                         APPLICATION NUMBER: US/08/256,003
FILING DATE: 11-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
                                                                                                                                                                                                                                                                                   ADDRESSEE: Chiron (
STREET: 4560 Hortor
CITY: Emeryville
STATE: California
COUNTRY: USA
ZIP: 94608-2916
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                                                                                                                                                                                                                                                                                                                                                                   4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                   Chiron Corporation
   (510)
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US-09-528-682-1 x US-08-256-003-5
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    Quality:
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; LOCATION:
US-08-256-003-5
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LENGTH: 711 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                            ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yrIleTyrValIleAlaThrAlaProAsnMetPheAsnValAsnAspVal 100
                                     CACAAGGTTGTGGAGATTCATCAAGAACAATCACAGGTGATACTTGTAAT
                                                         roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn
                                                                                                                                                                                            AGAAATCTGAATATAGCTCCGGCAGAGGATGGTTACAGATTAGCAGGTTT
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95.000
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488

167

117 288

338

247

84 197 67 147

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134

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; NAME/KEY:
; LOCATION:
US-09-044-696-1
                                                                                                   alignment_block:
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                                          Align seg 1/1
                                                                              US-09-528-682-1 x US-09-044-696-1
                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09044696
GENERAL INFORMATION:
APPLICANT: BARCHFELD, GAIL
APPLICANT: DEL GIUDICE, GIUSEPPE
APPLICANT: RAPPUOLI, RINO
TITLE OF INVENTION: DETOXIFIED MUTANTS OF BACTERIAL
TITLE OF INVENTION: ADP-RIBOSYLATING TOXINS AS PAREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (510) 655-35.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: HARBIN, ALISA A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 655-8730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,227
FILING DATE: 21-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 711 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 18-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CHIRON CORPORATION, INTELLECTUAL PROPERTY ADDRESSEE: R440
                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                       Quality: 1183.00
Ratio: 5.189
milarity: 95.000
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                                        US-09-044-696-1
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                                                                                                                                       Percent Identity:
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                                          from: 1
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seq_documentation_block:
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                                                                                                                                                Sequence
                                                                                                                               GENERAL INFORMATION:
                              TITLE OF INVENTION: TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                               689
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                                                                                                                                                                                                                                                                                                                 217 sValLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA 234
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                                                                                                                                                                                                                                               234 snArgIleArgAspGluLeu
                                                                                                                                                                                                                                                                                                                                                                                             201
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                                                                                                                                                                                             /cgn2_6/ptodata/2/pna/US082_COMB.seq:US-08-256-003-7
                                                                                                                                            Application US/08256003
                                                                                                               Domenighini, Mario
                            Immunogenic Detoxified Mutants of Cholera Toxin and of the Toxin Lt, Their Preparation and Their Use for the Preparation of Vaccines
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ADDRESSEE:

Chiron Corporation

STREET: 4560 Horton Street

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alignment_block:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, BARBARA G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       151
                                                                                                                                                                                                                                                                                                    101 GTACTCAAATGAATATCAACCTTTATGATCATGCAAGAGGAACTCAGACG
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MEDIUM TYPE: Floppy disk
   117
                                                                     101
                                                                                                      251
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                                                                                                                                                                     201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0
FILING DATE: 11-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                                                                                                                                                                                                   GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr 67
yGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyV 134
                                                    LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl 117
                                                                                                                                                                     AAGTGCCCACTTAGTGGGTCAAACTATATTGTCTGGTCATTCTACTTATT 250
                                                                                                                                                                                      GGATTTGTTAGGCACGATGATGGATATGTTTCCACCTCAATTAGTTTGAG
                                                                                                                                                                                                                                                                                                                                     lyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThrGlnThr 50
                                 TTAGGGGCATACAGTCCTCATCCAGATGAACAAGAAGTTTCTGCTTTAGG
                                                                                                   ATATATATGTTATAGCCACTGCACCCAACATGTTTAACGTTAATGATGTA 300
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seq_name: /cgn2_6/ptodata/2/pna/US090_COMB.seq:US-09-044-696-3
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                                                           PRIOR APPLICATION DATA:
APPLICATION UMBER: US 60/041,227
FILING DATE: 21-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: HARBIN, ALISA A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 1393.002
REFERENCE/TOCKET NUMBER: 1393.002
TELEPHONE: (510) 655-8730
TELEPHONE: (510) 655-8730
TELEPHONE: (510) 655-3542
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: EMERYVILLE
STATE: CALIFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: RAPPUOLI, RINO
TITLE OF INVENTION: DETOXIFIED MUTANTS OF BACTERIAL
TITLE OF INVENTION: ADP-RIBOSYLATING TOXINS AS PARENTERAL ADJUVANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 snArgIleArgAspGluLeu 240
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701 ATAGAATTAAGGATGAATTA 720
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LENGTH: 723 base pairs
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                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/044,696 FILING DATE: 18-MAR-1998 CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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nucleic acid
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US-09-528-682-1 x US-09-044-696-3
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Ratio: 4.814
Percent Similarity: 94.167
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LOCATION:
FEATURE:
NAME/KEY:
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                    GluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLy
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                                             CGCCGGGTTGTGGGAATGCTCCAAGATCATCGATCAGTAATACTTGCGAT
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alignment_block:
    US-09-528-682-1 x US-09-950-335A-1
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Percent Similarity:
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TITLE OF INVENTION: GENETICALLY ENGINEERED CO-EXPRESSION DNA VACCINES, CONSTRUCTIO
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: 4115-128
CURRENT APPLICATION NUMBER: US/09/950,335A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 723
TYPE: DNA
ORGANISM: Vibrio cholerae
ORGANISM: Vibrio cholerae
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alileAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyr
                                                                                                                                   LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl 117
                                                  yrīleTyrValīleAlaThrAlaProAsnMetPheAsnValAsnAspVal 100
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| AAGTGCCCACTTAGTGGGTCAAACTATATTGTCTGGTCATTCTACTTATT
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Ratio: 4.814
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seq_documentation_block:

Sequence 45, Application PC/TUS9930747

GENERAL INFORMATION:

APPLICANT: Boyce Thompson Institute for Plant Research at Cor
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Exp:
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427

CURRENT APPLICATION UNMBER: PCT/US99/30747

CURRENT APPLICATION UNMBER: PCT/US99/30747

SUTREENT SEQ ID NOS: 67

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 45
LENGTH: 777
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence:V. cholerae; OTHER INFORMATION: cholera toxin gene mutagenized to optimize ; OTHER INFORMATION: expression in plants. pcT-us99-30747-45
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Ratio: 4.814
milarity: 94.167
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/07694733 GENERAL INFORMATION:
                                                                                                                                                                                                                                          APPLICANT: Burnette, W. Neal APPLICANT: Kaslow, Harvey R. TITLE OF INVENTION: Recombinan TITLE OF INVENTION: Cholera TO NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      455
ZIP: 91320-1789

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in., D
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh OS 7.
SOFTWARE: Microsoft Word Version
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                                                                                                                                                              STREET: Amgen Center
STREET: 1840 Dehavilland
CITY: Thousand Oaks
                                                                                                                                         STATE: California
                                                                                                                      COUNTRY:
                                                                                                                                                                                                                           ADDRESSEE:
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704

654 200 604 554 167 504 150 454 134 404 354

304 84 254

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 19910502
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 1
SEQUIENCE CHARACTERISTICS:
LENGTH: 777 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double str
TOPOLOGY: CIrcular
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US-09-528-682-1 x US-07-694-733-1
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                GluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLy
                                            roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn 200
                                                                                                                                                                            AGTAACTTAGATATTGCTCCAGCAGCAGATGGTTATGGATTGGCAGGTTT
                                                                                                                                                                                            ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh 167
                                                                                                                                                                                                                                                                                                                        yGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyV 134
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Ratio: 4.814
milarity: 94.167
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Percent Identity:
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alignment_block:
US-09-528-682-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh OS 7.0.
SOFTWARE: Microsoft Word Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,605
FILING DATE: 05-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/694,733
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/694,733
FILING DATE: 02-MAY-1991
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 777 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-435-605-1
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APPLICANT: Kaslow, Harvey
TITLE OF INVENTION: Recomb
                                                                                                                         105
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MEDIUM TYPE: Diskette, 3.5 in.,
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CORRESPONDENCE ADDRESS:
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51 GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr
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STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
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TOPOLOGY: cir
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                                                      GTACTCAAATGAATATCAACCTTTATGATCATGCAAGAGGAACTCAGACG
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Ratio: 4.814
milarity: 94.167
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Percent Identity:
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seq_documentation_block:
Sequence 45, Application US/09470124
GENERAL INFORMATION:
APPLICANT: Mason
APPLICANT: Arntzen
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4866/84454
CURRENT APPLICATION NUMBER: US/09/470,124
CURRENT FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 45
LENGTH: 777
                                                                                                                                                                                                                                                                                                                                                        seq_name:
OTHER INFORMATION: Description of Artificial Sequence:V. cholerae OTHER INFORMATION: cholera toxin gene mutagenized to optimize OTHER INFORMATION: expression in plants.
                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                        FEATURE:
                                                                 NAME/KEY: CDS
LOCATION: (1)..(777)
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seq_name:

/cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:PCT-US97-11719-12

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alignment_block:
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                                                                                                                                       roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn
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                                        sValLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA
                                                                                                                                                                                 eProProAspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaP 184
                                                                                                                                                                                                                AGCAACTTGGACATTGCTCCAGCAGCAGGTTATGGATTGGCAGGTTT
                                                                                                                                                                                                                            ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh
                                                                                                                                                                                                                                                                      ATAGGATCAAGGATGAACTC
                   snArgIleArgAspGluLeu
                                                                                   GAAAAGACCCAATCTTTGGGTGTGAAGTTCCTTGATGAGTACCAATCTAA
                                                                                                                            CACCAGGTTGTGGAAATGCTCCAAGGTCAAGCATGAGCAACACTTGTGAT
                                                                                                                                                                       CCCTCCAGAGCATAGGGCTTGGAGGGAGGAGCCTTGGATTCACCATGCAC
                                                                                                                                                                                                                                                          TGCTTGATGAGCAACTCCATAGGAATAGGGGCTACAGGGATAGGTACTAC
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Ratio: 4.814
milarity: 94.167
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seq_documentation_block:
; Sequence 12, Application PC/TUS9711719
; GENERAL INFORMATION:
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US-09-528-682-1 x PCT-US97-11719-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/674,895 FILING DATE: 03-JUL-1996 INFORMATION FOR SEQ ID NO: 12:
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                                                                                                                                       1269 TTAGGGGCATACAGTCCTCATCCAGATGAACAAGAAGTTTCTGCTTTAGG
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134 alIleAspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyr 150
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HYPOTHETICAL: 1
ANTI-SENSE: NO
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APPLICATION NUMBER: PCT/US97/11719
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                      yGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyV 134
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                                                                                                                                                                    LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl 117

        yrIleTyrValIleAlaThrAlaProAsnMetPheAsnValAsnAspVal
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Ratio: 4.814
milarity: 94.167
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CONTAINING SPERM ANTIGEN, AND METHODS OF USE
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seq_documentation_block:
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                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/674,895

FILING DATE: 03-JUN-1996

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 529.0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 554-2337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12,
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GENERAL INFORMATION:
                                                                                                                                                     TELEFAX: (619) 554-6312 (NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1519
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10666 North Torrey Pines Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 snArgIleArgAspGluLeu 240
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TITLE OF INVENTION: CONTAINING SPERM ANTIGEN, AND METHODS OF USE
NUMBER OF SEQUENCES: 19
HYPOTHETICAL:
                                                                                                                            SEQUENCE CHARACTERISTICS:
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                      MOLECULE TYPE:
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                                                              STRANDEDNESS:
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                                              TOPOLOGY:
                                                                                                          LENGTH: 1956 base pairs
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alignment_block: US-09-528-682-1 \times US-08-674-895-12
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seq_documentation_block:
                       seq_name:
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Ratio: 4.814
Percent Similarity: 94.167
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                                                snargIleArgAspGluLeu 240
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ATAGAATTAAGGATGAATTA 168
                                                                                                             sValLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA 234
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                                                                                                 AGTTAAAAGACAAATATTTTCAGGCTATCAATCTGATATTGATACACATA 1668
                       /cgn2_6/ptodata/2/pna/US097B_COMB.seq:US-09-724-315-1
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CURRENT APPLICATION NUMBER: US/09/724,315;
CURRENT FILING DATE: 2000-11-27;
NUMBER OF SEQ ID NOS: 22;
SOFTWARE: PatentIn Ver. 2.1;
SEQ ID NO 1;
SEQ ID NO 1;
LENGTH: 5500;
TYPE: DNA;
ORGANISM: PDJV2002 plasmid
US-09-724-315-1
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    Quality:
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GENERAL INFORMATION:
APPLICANT: HAYNES, Joel R.
APPLICANT: ARRINGTON, Joshua
TITLE OF INVENTION: NUCLEIC ACID AI
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                                                                                                                                           ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh
                                                                                                                                                                                                             yGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyV 134
                                                                                                                                                                                                                                                                                                                     yrIleTyrValIleAlaThrAlaProAsnMetPheAsnValAsnAspVal 100
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roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn
                                       eProProAspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaP 184
                                                                                                                                                                                                TGGGATTCCATACTCCCAAATATATGGATGGTATCGAGTTCATTTTGGGG
                                                                                                                                                                                                                                                      TTAGGGGCATACAGTCCTCATCCAGATGAACAAGAAGTTTCTGCTTTAGG
                                                                                                                                                                                                                                                                                                         ATATATATGTTATAGCCACTGCACCCAACATGTTTAACGTTAATGATGTA
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4.814
94.167
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Percent Identity:
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alignment_block:
US-09-528-682-1
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                                                                                                                                Quality: 1088.00
Ratio: 4.814
Percent Similarity: 94.167
                                      Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6943 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Bicker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 00742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatibl
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for W
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FILING DATE: 26-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mekalanos, John J.
APPLICANT: Waldor, Matthew K.
TITLE OF INVENTION: NOVEL CHOI
TITLE OF INVENTION: AND METHOL
TITLE OF INVENTION: BACTERIA
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CITY: B
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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                                      to: US-08-670-974-6
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FastSEQ for Windows Version
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Identity:
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seq_documentation_block:
; Sequence 49, Application PC/TUS9930747
                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:PCT-US99-30747-49
                                                            GENERAL INFORMATION:
APPLICANT: Boyce Thompson Institute for Plant Research
TITLE OF INVENTION: Orally Immunogenic Bacterial Entero
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/8427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
SEQ ID
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 49
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alignment_block: US-09-528-682-1 x PCT-US99-30747-49
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PCT-US99-30747-49
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Quality: 1087.00
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Percent Similarity:
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NAME/KEY: CDS
LOCATION: (1)..(777)
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                                                                                  AGCAACTTGGACATTGCTCCAGCAGCAGATGGTTATGGATTGGCAGGTTT
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                                                                                                                                                                                                                                                                                                                                            yrileTyrVallleAlaThrAlaProAsnMetPheAsnValAsnAspVal 100
                                                        roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn 200
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                                    CACCAGGTTGTGGAAATGCTCCAAGGTCAAGCATGAGCAACACTTGTGAT 654
                                                                                                                                                       ArgasnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh
                                                                                                                                                                                                                               TGGAATCCCATACTCCCAAATCTATGGATGGTATAGGGTGCACTTTGGAG
                                                                                                                                                                                                                                                                               TTGGGAGCATACAGCCCTCACCCAGATGAGCAAGAGGTGTCTGCTTTGGG
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seq_documentation_block:
; Sequence 49, Application US/09470124
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Quality:
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FILE REFERENCE: 4868/4454
CURRENT APPLICATION NUMBER: US/09/470,124
CURRENT FILING DATE: 1999-12-24
RUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 49
LENGTH: 777
TYPE: DNA
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APPLICANT: Mason
APPLICANT: Arntzen
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LOCATION: (1)..(777)
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                                                                                         GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr
LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl 117
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                                               yrIleTyrValileAlaThrAlaProAsnMetPheAsnValAsnAspVal 100
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alignment_block:
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PCT-US99-30747-47
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                                                                       US-09-528-682-1 x PCT-US99-30747-47
                                       Align seg 1/1
                                                                                                                         Ratio:
Percent Similarity:
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GENERAL INFORMATION:

APPLICANT: Boyce Thompson Institute for Plant Research at Cor

TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins

TITLE OF INVENTION: Transgenic Plants

FILE REFERENCE: 4868/85427

CURRENT APPLICATION NUMBER: PCT/US99/30747

CURRENT FILLNG DATE: 1999-12-22

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 47
LENGTH: 777
                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial
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LOCATION: (1)..(777)
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Ratio: 4.796
milarity: 94.167
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                                                                                                                                                           Sequence 47, Application GENERAL INFORMATION:
APPLICANT: Mason
APPLICANT: Anntzen
APPLICANT: Anntzen
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/84454
CURRENT APPLICATION NUMBER: US/09/470,124
CURRENT FILLING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
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; OTHER INFORMATION: Description of Artificial Sequence:V. cholerae; OTHER INFORMATION: Cholera toxin gene mutagenized to optimize ; OTHER INFORMATION: expression in plants.
US-09-470-124-47
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Ratio: 4.796
Percent Similarity: 94.167
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LENGTH: 777
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LOCATION: (1)..(777)
FEATURE:
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NAME/KEY: CDS
LCCATION: (1)..(777)
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:V. cholerae
OTHER INFORMATION: cholera toxin gene mutagenized to optimize
OTHER INFORMATION: expression in plants.
PCT-US99-30747-51
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Quality:
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GENERAL INFORMATION:
APPLICANT: Boyce Thompson Institute for Plant Research at Cor TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins ITILE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427

CURRENT APPLICATION NUMBER: PCT/US99/30747

CURRENT ETLING DATE: 1999-12-22

NUMBER OF SEQ ID NOS: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 51
LENGTH: 777
TYPE: DNA
ORGANISM: Artificial Sequence
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101 LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl 117
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                                                                                                                                                                                                               51 GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr
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                                                         yrIleTyrValIleAlaThrAlaProAsnMetPheAsnValAsnAspVal 100
                                                                                                               GTACTCAGATGAACATCAACCTTTATGACCATGCAAGGGGAACTCAAACT
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OTHER INFORMATION: Description of Artificial Seque
; OTHER INFORMATION: cholera toxin gene mutagenized
; OTHER INFORMATION: expression in plants.
US-09-470-124-51
                                                        alignment_block:
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Align seg 1/1
                                    US-09-528-682-1 x US-09-470-124-51
                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/470,124
CURRENT FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 51
LENGTH: 777
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 51, Application US/09470124 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(777)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed TITLE OF INVENTION: Transgenic Plants FILE REFERENCE: 4868/84454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Arntzen
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                                                                                          Quality: 1081.00
Ratio: 4.804
milarity: 93.750
to: US-09-470-124-51
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from:
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Identity:
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to:
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seq_documentation_block:

755

ATAGGATCAAGGATGAACTC

774

Sequence 3, Application US/09724315; GENERAL INFORMATION:

APPLICANT: HAYNES, JOEL R.
APPLICANT: ARRINGTON, JOENUA
TITLE OF INVENTION: NUCLEIC ACID ADJUVANTS
FILE REFERENCE: APF41
FULRERNT APPLICATION NUMBER: US/09/724,315
CURRENT FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 22

SOFTWARE:

PatentIn

Ver.

seq_name: /cgn2_6/ptodata/2/pna/US097B_COMB.seq:US-09-724-315-3

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234 snArgIleArgAspGluLeu 240
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|TGCTTGATGAGCAACTCCATAGGAATAGGGGCTACAGGGATAGGTACTAC
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|CAATCAGGTGGTCTTATGCCAAGGGGACAATCTGAGTACTTTGACAGGG
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                                    GGTGAAGAGGCAAATCTTCTCAGGCTACCAATCTGACATTGACACCCCACA
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; SEQ ID NO 3; LENCTH: 5488; TYPE: DNA; ORGANISM: plasmid ppJV2006 US-09-724-315-3
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US-09-528-682-1 x US-09-724-315-3
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Ratio: 4.824
Percent Similarity: 94.068
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             217 sValLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA 234
                                                                      201 GluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLy
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                                                                                                              CGCCGGGTTGTGGGAATGCTCCAAGATCATCGATGAGTAATACTTGCGAT
                                                                                                                                                                    CCCTCCGGAGCATAGAGCTTGGAGGGGAAGAGCCGTGGATTCATCATGCAC
AGTTAAAAGACAAATATTTTCAGGCTATCAATCTGATATTGATACACATA
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Gaps:
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alignment_block:
US-09-528-682-1 x PCT-US01-08582-1
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Quality: 1053.00
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                                                                                                                                                                                                                                                                                                                                                         Ratio: 4.701
Percent Similarity:, 93.333
                                                                                                                                                                                                                                                                    Align seg 1/1 to: PCT-US01-08582-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application PC/TUS0108582
GENERAL INFORMATION:
GENERAL TOTAL TOTAL ON THE APPLICANT: UAB Research Foundation
TITLE OF INVENTION: Chimeric Nontoxic Mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4675 ATAGAATT 4682
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                                                         34 lyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThrGlnThr
 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
SOFTWARE: Patentin Release #1.0, Vers
APPLICATION NUMBER: PCT/US01/08582
FILING DATE: 16-Mar-2001
CLASSIFICATION: CLASSIFICATION:
NAME: Hendricks, Glenna
TORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: McG-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/425-8405
TELEFAX: 703/425-8406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: Hendricks and Assoc
                                     GTACTCAAATGAATATCAACCTTTATGATCATGCAAGAGGAACTCAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: VA
COUNTRY: US
ZIP: 22031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2022 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Fairfax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P.O. Box 2509
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Percent Identity:
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Gaps:

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seq_documentation_block:
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GENERAL INFORMATION:
APPLICANT: UAB Research Foundation
TITLE OF INVENTION: Chimeric Nonto)
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                                                                    ZIP: 22031

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eProProAspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaP 184
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                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
APPLICATION NUMBER: PCT/US01/08582 FILING DATE: 16-Mar-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                              COUNTRY: US
                                                                                                                                                                                                                  STATE: VA
                                                                                                                                                                                                                                  CITY: Fairfax
                                                                                                                                                                                                                                                      STREET: P.O. Box 2509
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INFORMATION FOR SEQ ID NO:
                                                                        1021
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                                eProProAspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaP 184
                                                                                        ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh 167
                                                                                                                                                                                                                                                                                                                                                                                                            yrIleTyrValIleAlaThrAlaProAsnMetPheAsnValAsnAspVal 100
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2022 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: McG-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/425-8405
TELEFAX: 703/425-8406
                                                                        AGTAACTTAGATATTGCTCCAGCAGCAGATGGTTATGGATTGGCAGGTTT
                                                                                                                                                     TGGGATTCCATACTCCCAAATATATGGATGGTATCGAGTTCATTTTGGGG
                                                                                                                                                                                                                                                                                                                                                                                          ATATATATGTTATAGCCACTGCACCCAACATGTTTAACGTTAATGATGA. 870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
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93.333
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TITLE OF INVENTION: GENETICALLY ENGINEERED CO
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 415-128
CURRENT APPLICATION NUMBER: US/09/950,335A
CURRENT FILLING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIA VERSION 3.1
SEQ ID NO 2
LENGTH: 582
TYPE: DNA
CORGANISM: Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09950335A GENERAL INFORMATION:
APPLICANT: HONE, DAVID M.
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|AGTGCCCACTTAGTGGGTCAAACTATATTGTCTGGTCATTCTACTTATT
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CGCCGGGTTGTGGGAATGCTCCAAGATCATCGATGAGTAATACTTGCGAT 1170
                                                                               yrileTyrValileAlaThrAlaProAsnMetPheAsnValAsnAspVal 100
                                                                                                                                                                                                                      GlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuAr
                                                                                                                                                                                                                                                                                        lyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThrGlnThr 50
                                                                                                                                                                                                                                                                                                                                                                             sArgSerGlyGlyLeuMetProArgGlyHisAsnGluTyrPheAspArgG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAGAATTAAGGATGAATTA 1290
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                                                    ATATATATGTTATAGCCACTGCACCCAACATGTTTAACGTTAATGATGTA
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Ratio:
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alignment_block:
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                                                                                                                                                                                                                                                                                                       PCT-US01-16904-1
                                                                                                                            Align seg 1/1 to:
                                                                                                                                                           US-09-528-682-1 x PCT-US01-16904-1
                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0 SEQ ID NO 1 LENGTH: 7586
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                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (6184)...(6184)
OTHER INFORMATION: n can b
NAME/KEY: misc_feature
LOCATION: (6226)...(7053)
OTHER INFORMATION: n can b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Methods for Introducing and Expressing Genes in Animal Cells, TITLE OF INVENTION: Bacterial Blebs for Use in Same FILE REFERENCE: 4115-121 PCT CURRENT APPLICATION NUMBER: PCT/US01/16904 CURRENT FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 60/206,994 PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Powell, Robert J. APPLICANT: Hone, David M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: University of Maryland Biotechnology Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: (6224)..(6224) OTHER INFORMATION: n can
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Cholera Toxin Al Subunit Sequence
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roGlnGlyCysGlyAsnSerSerArgThr 193
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; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Recombinant DNA
US-09-402-100-1
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                                                                                                                                                                                FILE REFERENCE: 0136/06140
CURRENT APPLICATION NUMBER: US/09/402,100
CURRENT FILING DATE: 1999-09-27
EARLIER APPLICATION NUMBER: KR 97-11950
EARLIER FILING DATE: 1997-03-31
EARLIER APPLICATION NUMBER: KR 97-11951
EARLIER FILING DATE: 1997-03-31
NUMBER OF SEQ ID NOS: 48
NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09402100 GENERAL INFORMATION:
                                                                                                                                                   SOFTWARE: PatentIn version 3.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                            APPLICANT: Yu, Young-Hyo
APPLICANT: Park, Myung-Hwan
APPLICANT: Choi, Deok-Joon
APPLICANT: Jung, Hyung-Jin
TITLE OF INVENTION: Recombinant Microorganisms Expressing Antigenic Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kim, Byung-O
APPLICANT: Shin, Sung-Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Daewoong Pharmaceutical Co,
                                                                           FEATURE:
                                                                                             ORGANISM: Artificial Sequence
                                                                                                                TYPE: DNA
                                                                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               509
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Yu, Young-Hyo
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alignment_block:
US-09-528-682-1 x US-09-402-100-1
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APPLICANT: Choi, Deck-Joon
APPLICANT: Choi, Deck-Joon
APPLICANT: Choi, Deck-Joon
TITLE OF INVENTION: Recombinant Microorganisms Ex
FILE REFERENCE: 0136/06140
CURRENT APPLICATION NUMBER: US/09/402,100
CURRENT FILING DATE: 1999-09-27
EARLIER APPLICATION NUMBER: KR 97-11950
EARLIER FILING DATE: 1997-03-31
EARLIER FILING DATE: 1997-03-31
EARLIER FILING DATE: 1997-03-31
NUMBER OF SEQ ID NOS: 48
COMMUNICATION NUMBER: KR 97-11951
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Ratio:
Percent Similarity:
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                                                                                                                              SEQ ID NO 3
LENGTH: 4149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09402100
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yu, Young-Hyo
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                                                                                                                                                                           SOFTWARE: PatentIn
LOCATION: ()..()
OTHER INFORMATION: Recombinant DNA
                                    FEATURE:
NAME/KEY: misc_feature
                                                                                                         TYPE: DNA
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                                                                                   ORGANISM: Artificial Sequence
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Gaps:
Percent Identity:
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alignment_scores:

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APPLICANT: Park, Seung-Rook
APPLICANT: Yu, Young-Hyo
TITLE OF INVENTION: A RECOMBINANT MICROORGANISM EXI
TITLE OF INVENTION: A RECOMBINANT MICROORGANISM EXI
TITLE OF INVENTION: AN ANTIGENIC PROTEIN, ADHESIN
FILE REFERENCE: 0136/02164
CURRENT APPLICATION NUMBER: US/09/051,315
CURRENT FILING DATE: 1998-04-03
EARLIER APPLICATION NUMBER: DCT/KR 97/00091
EARLIER FILING DATE: 1997-05-21
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-528-682-1 x US-09-402-100-3
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US-09-528-682-1 x US-09-051-315-1
                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-051-315-1
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                                                                                                                                           Align seg 1/1 to: US-09-051-315-1
                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
LENGTH: 1516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Daewoong Pharmaceutical APPLICANT: Kim, Byung-O APPLICANT: Lee, Byung-Kwang APPLICANT: Yoon, Suk-Won
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                            17 sArgSerGlyGlyLeuMet.....
                                                                                                     1 AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy 17
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ATCAGAACCCGGGTTATTATTCTCCACCGGTTTGGACAAAATGGAAGGGG 502
                                                                     AATGGCGAAATTGTTTTACGCCCCGATCCTAAAAGGACCATACAGAAAAA 452
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                                                                                                                                                                                                                              Length: 263
Gaps: 6
Percent Identity: 26.996
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Sequence 1, Application US/09423493

GENERAL INFORMATION:
APPLICANT: DAEWONG PHARMACEUTICAL CO., LTD
APPLICANT: Kim, B.O., et al.
APPLICANT: Kim, B.O., et al.
TITLE OF INVENTION: A preventive and therapeutic vaccine for TITLE OF INVENTION: Heliobacter Pylori-associated diseases.
FILE REFERENCE: 0136/06320
CURRENT APPLICATION NUMBER: US/09/423,493
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: BCT/KR98/00072
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 6
SOFTMARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/pna/US094_COMB.seq:US-09-423-493-1
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; OTHER INFORMATION: Fusion oligonucleotide between Heliobacter pylori; OTHER INFORMATION: and Vibrio cholerae US-09-423-493-1
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US-09-528-682-1 x US-09-423-493-1
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                        ProTrpIleHisHisAlaProGlnGlyCysGlyAsnSerSerArgThrIl 194
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Gaps: 6
Percent Identity: 26.996
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alignment_block:
US-09-528-682-1 x US-09-760-234-1
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Quality:
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PRIOR FILING DATE: 1997-05-21
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1516
TYPE: DNA
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CURRENT APPLICATION NUMBER: US/09/760,234
CURRENT FILING DATE: 2001-01-11
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TITLE OF INVENTION: A RECOMBINANT MICROORGANISM EXPRESSING
TITLE OF INVENTION: AN ANTIGENIC PROTEIN, ADHESIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/051,315 PRIOR FILING DATE: 1998-04-03
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APPLICANT: Lee, Byoung-Kwang
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: DNA sequence of a fusion gene prepared by ligating
OTHER INFORMATION: adhesin gene of H. pylori and A2 and B subunit genes of
OTHER INFORMATION: Vibrio cholerae toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                    453 ATCAGAACCCGGGTTATTATTCTCCACCGGTTTGGACAAAATGGAAGGGG 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 euArgGluTyrGlnSerLysValLysArgGlnIlePheSerAspTyrGln 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 873 GATCAGTAATACTTGCGATGAAAAAACCCCAAAGTCTAGGTGTAAAATTCC
                                                                                                                                                                                                 503 TTTTAATCCCGGCTGGGTTTATTAAGGTTACCATACTAGAGCCTATGAGT 552
                                                                                                                                                                                                                                                                                                                                                                                                     403 AATGGCGAAATTGTTTTACGCCCCGATCCTAAAAGGACCATACAGAAAAA 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               973 TCTGATATTGATACACATAATAGAATTAAGGATGAATTA 1011
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                                         44 sAlaArgGlyThrGlnThrGlyPheValArgTyrAspAspGlyTyrValS 61
                                                                                                                                          28 AsnGluTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHi 44
                                                                                                                                                                                                                                              24 ......ProArgGly.....His
                                                                                                                                                                                                                                                                                                                                                    17 sArgSerGlyGlyLeuMet.....
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy 17
GGGGAATCTTTGGATTCTTTTACGATGGATTTGAGCGAGTTGGACATTCA
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Park, Seung-Kook
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-760-234-1
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1.963
46.768
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Percent Identity:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application:
SOFTWARE: Patentin Release #1:0, Ve CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,438
FILING DATE: 08-OCT-193
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: US 06/472,276
FILING DATE: 04-MAR-1983
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & McKenzle
STREET: Suite 1100, 815 Connecticut Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LEVINE, MYRON M.
TITLE OF INVENTION: VIBRIO CHOLERAE NON-01 SEROGROUP VACCINE
TITLE OF INVENTION: STRAINS, METHODS OF MAKING SAME AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94
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                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 20006-4078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrArgValAsnPheGlyValIleAspGluArgLeuHisArgAsnArgGl 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATCAGTAATACTTGCGATGAAAAAACCCAAAGTCTAGGTGTAAAAATTCC 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProTrpIleH1sH1sAlaProGlnGlyCysGlyAsnSerSerArgThrIl 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lyTyrArgLeuAlaGlyPheProProAspHisGlnAlaTrpArgGluGlu 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTC.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerGlyTyrSerThrTyrTyrIleTyrValIleAlaThrAlaProAsnMe 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCACT....ATGGTTAAGGGAACGGATAATTCTAATGACGCGATCAAG 696
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                                                                                                                                                                                                                                                                                                                                                 Washington
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                                                                                                                                                             Version
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alignment_block:
US-09-528-682-1 x US-08-133-438-3/rev
                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/pna/US081_COMB.seq:US-08-133-439-3
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Percent Similarity:
                                                                                                     Sequence 3, Application US/08133439 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                        1339 TCTAGAGCGATCAGT...AATACTTGCGATGAAAAAACCCAAAGTCTAGG
                                                                                                                                                                                                                                   1242 CAGGCTATCAATCTGATATTGATACACATAATAGAATTAAGGATGAATTA 1193
                                                                                                                                                                                                                                                                                                                     1292 TGTAAAATTCCTTGACGAATACCAATCTAAAGTTAAAAGACAAATATTTT 1243
APPLICANT: KAPER, James B.
APPLICANT: LEVINE, MYTON M.
TITLE OF INVENTION: VIBRIO CHOLERAE CVD111, ME
TITLE OF INVENTION: SAME, AND VACCINE DERIVED
NUMBER OF SEQUENCES: 3
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REFERENCE/DOCKET NUMBER: BAN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 452-7000
TELERAX: (202) 452-7074
TELEX: RASS?
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FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/931,943
FILING DATE: 12-AUG-1992
                                                                                                                                                                                                                                                                                                                                           207 rThrIleTyrLeuArgGluTyrGlnSerLysValLysArgGlnIlePheS 224
                                                                                                                                                                                                                                                                                                                                                                                                                            191 SerArgThrIleThrGlyAspThrCysAsnGluGluThrGlnAsnLeuSe 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/363,383
FILING DATE: 05-JUN-1989
                                                                                                                                                                                                                                                     224 erAspTyrGlnSerGluValAspIleTyrAsnArgIleArgAspGluLeu 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/581,406
FILING DATE: 17-FEB-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kile, Bradford E. REGISTRATION NUMBER: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
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3.567
90.000
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Percent Identity:
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                                         METHOD OF MAKING
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                      Align seg 1/1 to reverse of: US-08-133-439-3 from: 1
                                                                                                                                                                                                                              US-09-528-682-1 x US-08-133-439-3/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 89552
INFORMATION FOR SEQ ID NO:
191 SerArgThrIleThrGlyAspThrCysAsnGluGluThrGlnAsnLeuSe 207
||||||:::|||:::|||:::|||:::||||:::||||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::|:::||:::||:::||:::|:::||:::||:::||:::||:::|:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:
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ORGANISM: Vibrio cholerae
STRAIN: CVD110
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 00
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Baker & McKenzie
STREET: Suite 1100, 815 Connecticut Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO
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MOLECULE TYPE: DNA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 04-MAR-
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OPERATING SYSTEM: PC-DOS/MS-DOS
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EDNESS: double
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12-AUG-1992
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3.567
90.000
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seq_documentation_block:
; Sequence 13, Application US/09771536B
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US-09-528-682-1 x US-09-771-536B-15
                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/pna/US097C_COMB.seq:US-09-771-536B-13
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SEQ ID NO 15
LENGTH: 651
                                                                                                                                                                                                                                    GENERAL INFORMATION:
SEQ ID NO 13
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                                      APPLICANT: Yu, Jie
APPLICANT: Arakawa, Takeshi
TITLE OF INVENTION: Transgenic Plant-Based Vaccines
FILE REFERENCE: 12273-3
CURRENT FAPLICATION NUMBER: US/09/771,536B
CURRENT FILLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 15
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APPLICANT: Arakawa, Takeshi
TITLE OF INVENTION: Transgenic Plant-Based Vaccines
FILE REFERENCE: 12273-3
CURRENT APPLICATION NUMBER: US/09/771,536B
CURRENT FILING DATE: 2001-01-29
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                     SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                       Langridge, William H. R.
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alignment_block:
us-09-528-682-1 x us-09-771-536B-13
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Quality:
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TYPE: DNA
; ORGANISM: Vibrio cholerae
US-09-771-536B-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/pna/US092_COMB.seq:US-09-255-829-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-09-771-536B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/09255829 GENERAL INFORMATION:
                                                                                             TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                 NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/255,829
FILING DATE: 23-FEB-1999
PRIOR APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 22-AUG-1997
                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/782,893
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 AspThrCysAsnGluGluThrGlnAsnLeuSerThrIleTyrLeuArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AATACTTGCGATGAAAAACCCAAAGTCTAGGTGTAAAATTCCTTGACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
                                                                           LENGTH:
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                                nucleic acid
DEDNESS: double
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                  linear
DNA (genomic)
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3.925
90.909
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                                                                                                                                                                                              1581.0130002
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: 0
: 65.909
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; FEATURE:
; NAME/KEY:
; LOCATION:
US-09-255-829-15
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US-09-528-682-1 x US-09-582-034-2
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: C. elegans
US-09-582-034-2
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US-09-528-682-1 x US-09-255-829-15
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Percent Similarity:
                                                                                                                                                                                  Align seg 1/1 to: US-09-582-034-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09582034
GENERAL INFORMATION:
APPLICANT: Napler, Johnathan A.
APPLICANT: Michaelson, Louise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/582,034
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: PCT/GB98/03895
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: UX 9814034.6
PRIOR FILING DATE: 1998-06-29
PRIOR PRIOR APPLICATION NUMBER: UX 9727256.1
PRIOR EILING DATE: 1997-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Stobart, Keith TITLE OF INVENTION: Desaturase FILE REFERENCE: 00487.00003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2696 CACATAATAGAATTAAGGATGAATTA 2721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2646 ATCTAAAGTTAAAAGACAAATATTTTCAGGCTATCAATCTGATATTGATA 2695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2596 AATCAAAGATTATTATCTACATTTACTGAATATATTAAGTCTAGGCCTCA 2645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                          328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 leTyrAsnArgIleArgAspGluLeu 240
369 TGGATCTCCTTTGTTCTACATTAGAAAAATT.....CTTGAAACAATCT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 AsnGluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyr...Gl 215
                                          78 rGlyTyrSerThrTyrTyrIleTyrValIleAlaThrAlaProAsnMetP 95
                                                                                                                                     62 ThrSerLeuSerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSe 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
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52.747
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3.318
78.571
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Percent Identity:
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                                                                                          GTTCGTGCAGAAGGACTTATGGA 368
                                                                                                                                                                                  from: 1 to: 1344
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26.374
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alignment_block:
US-09-528-682-1 x PCT-US99-28655-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LENGTH: 1461
; TYPE: DNA
; ORGANIZM: Caenorhabditis elegans
PCT-US99-28655-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
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                                                                                                                                                                    Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application PC/TUS9928655
GENERAL INFORMATION:
APPLICANT: Browse, John et al.
TITLE OF INVENTION: Desaturases and Methods of Using Them for Synthesis
TITLE OF INVENTION: Polyunsaturated Fatty Acids
FILE REFERENCE: 53860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: PCT/US99/28655
CURRENT FILING DATE: 1999-12-06
EARLIER APPLICATION NUMBER: 60/111,301
EARLIER FILING DATE: 1998-12-07
NUMBER OF SEO ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 1
                                               370 ACTGATCTACGTATGCGA.....GTTCGTGCAGAAGGACTTATGGA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             771 GACATTCATGTTACCATTCCTCCGTCTCTCGTGGCTTCTTCAGT 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 uProTrpIleHisHisAla.ProGlnGlyCysGlyAsnSerSerArgThr 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 GlyTyrArgLeuAlaGlyPheProProAspHisGlnAlaTrpArgGluGi 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   533 TGTTCAAAAACAGATACTACAATGATTTG.....GCCAGCTATTTCGTT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       721 TCTCAGGATTCATGGGTTATGACTCTATTCAGATGGCAACATGTTCATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 IleThrGlyAspThrCysAsnGluGluThrGlnAsnLeuSerThrIleTy 210
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78 rGlyTyrSerThrTyrTyrIleTyrValIleAlaThrAlaProAsnMetP 95
                                                                                                      62 ThrSerLeuSerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSe
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                                                                                                                                                                                                                                                                                                                                                        Quality:
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                                                                                                                                                                 PCT-US99-28655-1
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1.036
52.747
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Gaps:
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of.

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alignment_block:
                                                                                                                                                                                        alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                  ; ORGANISM: Caenorhabditis elegans US-09-857-583-1
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                                                     US-09-528-682-1 x US-09-857-583-1
Align seg 1/1 to: US-09-857-583-1
                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09857583

Sequence 1, Application US/09857583

GENERAL INFORMATION:
APPLICANT: Browse, John et al.
APPLICANT: Browse, John et al.
TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF POLYUNS
TITLE OF INVENTION: FATTY ACIDS
FILE REFERENCE: 4630-58963
CURRENT APPLICATION NUMBER: US/09/857,583
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/111,301
PRIOR FILING DATE: 1998-12-07
                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn versi
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/US99/28655
PRIOR FILING DATE: 1999-12-06
                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 IleThrGlyAspThrCysAsnGluGluThrGlnAsnLeuSerThrIleTy 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 GlyTyrArgLeuAlaGlyPheProProAspHisGlnAlaTrpArgGluGl 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACATTCATGTTACCATTCCTCCGTCTCTCGTGGCTTCTTCAGT
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                                                                                                                                                            Ratio:
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1.036
52.747
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Percent Identity:
  from: 1
  to: 1461
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11
26.374
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08245848 GENERAL INFORMATION:
APPLICATION NUMBER: US/08/245,848
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,212
FILING DATE: 29-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LODEL, YVES
TITLE OF INVENTION: Novel Vaccine
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp.
STREET: P.O. Box 1539
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Locht, Camille APPLICANT: Lobet, Yves
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                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 19406-0939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnGluValSerAlaLeuGlyGlyIleProTyrSerGlnIleTyrGlyTr 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTCAGGATTCATGGGTTATGACTCTATTCAGATGGCAACATGTTCATTG 812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTTCAAAAACAGATACTACAATGATTTG.....GCCAGCTATTTCGTT 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pTyrArgValAsnPheGlyValIleAspGluArgLeuHisArgAsnArgG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTCCATCAGCTATTCTAATGGGAGTTGCGTGGCAACAATTG...GGATG 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrSerLeuSerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSe
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                                                                                                                                                                                                       Version
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alignment_block:
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Quality:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1i
MOLECULE TYPE:
HYPOTHETICAL:
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LENGTH: 4207 base pairs
TYPE: nucleic acid
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TELEPHONE: 215 270 5024
                                                                        936
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                                  157
                                                                                                                                                                              123 nIleTyrGlyTrpTyrArgValAsnPheGlyValIleAspGluArgLeuH 140
                                                                                                                                                                                                                                                    107 HisProTyrGluGlnGluValSerAlaLeuGlyGlyIleProTyrSerGl 123
                                                                                                                                                                                                                                                                                                                                                                  844 GGGGC....ACCGGCCACTTCATCGGCTACATCTACGAAGTCCGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                        794 CTATCTCGAACATCGCATGCAGGAAGCGTTCGAGGCCGAACGCGCCGGCA 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  744 AGCAACAGCGCTTTCGTCTCCACCAGCAGCAGCCGGCGCTATACCGAGGT 793
                                                                                                                                                                                                                                                                                                               91 AlaProAsnMetPheAsnValAsnAsp..ValLeuGlyValTyrSerPro 106
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                                                                                                                                                                                                                                                                                                                                                                                                  74 InSerIleLeuSerGlyTyrSerThrTyrTyrIleTyrValIleAlaThr 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sutton, Jeffrey A REGISTRATION NUMBER: 34
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                    ProAlaGluAspGlyTyrArgLeuAlaGlyPheProProAspHisGlnAl 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ....AATGTGCTCGACCATCTGACCGGACGTTCCTGCCAGGTCGGCAGC 743
                                                                      isArgAsnArgGluTyrArgAspArgTyrTyrArgAsnLeuAsnIleAla 156
                                                                                                                                      ......CGTCGAC
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.CGAATATCTGGCACACCGCCG...CATTCCGC 1020
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Percent Identity:
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24.424
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173 aTrpArgGluGluProTrpIleHisHisAlaProGlnGlyCysGlyAsnS 190

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seq_documentation_block:
; Sequence 3096, Applica
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    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Agrobacterium tumefaciens US-09-514-000-3096
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SEQ ID NO 3096
LENGTH: 1671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15490)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/514,000 CURRENT FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hinkle, Gregory J. APPLICANT: Slater, Steven C.
                                                                                                                                                                      1010
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130 lAsnPheGlyValIleAspGluArgLeuHisArgAsnArgGluTyrArgA 147
                                                                                                                                                                                                                                                                                                                                                                                        910 GAGAATCTTGATGCGCGCCTTGTATTTGTTGTCGCGGCGGCGGTGCAGGT 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      837
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                                                      GCCGACGTAAACGGCAAAACCGATCTCACCCTTGTCGTTCTTTTTCAGAT 1109
                                                                                                       SerGinIleTyrGly......TrpTyrArgVa 130
                                                                                                                                                                 AGGAAGTCGCGAATCTTCTTGGCGATCATCGGCGTACGGCCCTGCCCGCC 1059
                                                                                                                                                                                                                       lnGluValSerAlaLeuGlyGly......1leProTyr 121
                                                                                                                                                                                                                                                                              TATAAACGCGCATGACGGCCGTGGTATAGGACAGCAGGTCCTCTTCCGGC 1009
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Gaps: 12
Percent Identity: 22.358
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APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

TITLE OF INVENTION: Agrobacterium tumefaciens Genome Seq.

FILE REFERENCE: 38-10(15490)C

CURRENT APPLICATION NUMBER: US/09/739,449

CURRENT FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: US 09/514,000

PRIOR FILING DATE: 2000-02-23

NUMBER OF SEQ ID NOS: 13351

SEQ ID NO 5019

LENGTH: 1671

TYPE: DNA

CROANIEW. Archarterium tumofacions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
; Sequence 5019, Application US/09739449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/pna/US097B_COMB.seq:US-09-739-449-5019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: US-09-739-449-5019
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                                                                                                                                                                                                                                                                                              911 CCTTCAGGGGGGTCTTTCAGCGCCGGGGGGGGAAAT.....A
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                       33 rg.GlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThrGl 49
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                                                                                                                                           nThrGlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerL 66
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seq_documentation_block:

Sequence 5019, Application US/09803110

GENERAL INFORMATION:

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

TITLE OF INVENTION: Agrobacterium tumefaciens Genome Seq:

FILE REFERENCE: 38-10(15490)D

CURRENT APPLICATION NUMBER: US/09/803,110

CURRENT FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: US 09/739,449

PRIOR FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: US 09/514,000

PRIOR FILING DATE: 2000-02-23

PRIOR APPLICATION NUMBER: US 09/514,000

PRIOR FILING DATE: 1999-12-01

NUMBER OF SEQ ID NOS: 13351
alignment_block:
US-09-528-682-1 x US-09-803-110-5019/rev
                                                                                                                 alignment_scores:
Quality:
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                                                                     Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SEQ ID NO 5019
LENGTH: 1671
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Percent Identity:
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seq_documentation_block:
   Sequence 1915, Application US/60168139
   GENERAL INFORMATION:
                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/pna/US6016_COMB.seq:US-60-168-139-1915
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                APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequence And Uses Thereof
FILE REFERENCE: 38-21(15490)A
CURRENT APPLICATION NUMBER: US/60/168,139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               961 AACGGGCAAAACCTTCATCCGCACGCTTCCAGCGCGCCAGGCTTTCCCAG
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                                                                                                                                                                                                                                               TTCCACGCTTGCCAGTTCAGAGAGATATCCGGCGT
                                                                                                                                                                                                                                                                                                                                                                                  leThrGlyAspThrCysAsnGluGluThrGlnAsnLeuSerThrIleTyr 210
                                                                                                                                                                                                                                                                                                                                                                                                                               CGACTTCGTC.....TGCGGCAGCACCCGCGAAATGA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uProTrpIleHisHisAlaProGlnGlyCysGlyAsnSerSerArgThrI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGCACGGAAGACCATTGACGCAGGATTTCCGCATAGGGACGCGGATCGG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCACCCGTCACCGCGATCTTGAACTTGCGCGGCAGGAACGAGAATTCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spargTyrTyrargasnLeuAsnIleAlaProAlaGluAspGlyTyrarg 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGGCCGATATCGTGGAC.....CTGAATGGCGGCGCGCGCTCGCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lAsnPheGlyValIleAspGluArgLeuHisArgAsnArgGluTyrArgA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGACGTAAACGGCAAAACCGATCTCACCCTTGTCGTTCTTTTCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerGlnIleTyrGly......TrpTyrArgVa 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATAAACGCGCATGACGGCCGTGGTATAGGACAGCAGGTCCTCTTCCGGC 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tPheAsnValAsnAspValLeuGlyValTyrSerProHisProTyrGluG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGAATCTTGATGCGCGCCTTGTATTTGTTGTCGCGGCGGCCGTGCAGGT 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....SerThrTyrTyrIleTyrValIleAlaThrAlaProAsnMe 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATTCAACCTCGACCTGGCGGGCCAGTTCTTCTGCGCCGGTTTCATGTAC 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyTyr.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTCGGTGTTTTCAG......CTCCGCG 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCGGTGATGGCGGCAATATCGGCATC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuAlaGlyPheProProAspHisGln.....AlaTrpArgGluGl 177
                                                                                                                                                                                                                                                                                                                                        220
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alignment_block:
US-09-528-682-1 x US-60-168-139-1915/rev
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; TYPE: DNA
; ORGANIZM: Agrobacterium tumefaciens
US-60-168-139-1915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 3432
SEQ ID NO 1915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1229 TATAAACGCGCATGACGGCCGTGGTATAGGACAGCAGGTCCTCTTCCGGC 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1478 AACGGCCAAAACCTTCATCCGCACGCTTCCAGCGCGCCAGGCTTTCCCAG 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                lAsnPheGlyValIleAspGluArgLeuHisArgAsnArgGluTyrArgA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATTCAACCTCGACCTGGCGGGCCAGTTCTTCTGCGCCGGTTTCATGTAC 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTCGGTGTTTTTCAG......CTCCGCG 1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sArgSerGlyGlyLeu...MetProArgGlyHisAsnGluTyrPheAspA 33
: :::|||||||| |||
  leThrGlyAspThrCysAsnGluGluThrGlnAsnLeuSerThrIleTyr 210
                                                                                                                                                                                                                               LeuAlaGlyPheProProAspHisGln......AlaTrpArgGluGl 177
                                                                                                                                                                                                                                                                                               GCACCCGTCACCGCGATCTTGAACTTGCGCGGCAGGAACGAGAATTCCGG
                                                                                                                                                                                                                                                                                                                                                 spArgTyrTyrArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArg 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lnGluValSerAlaLeuGlyGly......IleProTyr 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGAATCTTGATGCGCGCCTTGTATTTGTTGTCGCGGCGGCCGTGCAGGT 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                euArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyTyr..... 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nThrGlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rg.GlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThrGl 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGACTTCGTC.....TGCGGCAGCACCCGCGAAATGA
                                                                                                                                uProTrpIleHisHisAlaProGlnGlyCysGlyAsnSerSerArgThrI 194
                                                                                                                                                                                        ATGCACGGAAGACCATTGACGCAGGATTTCCGCATAGGGACGCGGATCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCGACGTAAACGGCAAAACCGATCTCACCCTTGTCGTTCTTTTTCAGAT 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerGlnIleTyrGly.....TrpTyrArgVa 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGAAGTCGCGAATCTTCTTGGCGATCATCGGCGTACGGCCCTGCCCGCC 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tPheAsnValAsnAspValLeuGlyValTyrSerProHisProTyrGluG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCGGTGATGGCGGCAATATCGGCATC......CGGCAGCTTCA 1353
                                                                                                                                                                                                                                                                                                                                                                                                         GCAGGCCGATATCGTGGAC.....CTGAATGGCGGCGCGCGCTCGCTCG 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....SerThrTyrTyrIleTyrValIleAlaThrAlaProAsnMe 94
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50.813
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Gaps: 12
Percent Identity: 22.358
904
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alignment_block:
US-09-528-682-1 x US-09-620-392-45559
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; ORGANISM: Oryza
US-09-620-392-45559
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; Sequence 45559, Applic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:US-09-620-392-45559
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Percent Similarity:
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SEQ ID NO 45559
LENGTH: 7412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof FILE REFERENCE: 38-21(51237)E
CURRENT APPLICATION NUMBER: US/09/620,392
CURRENT FILING DATE: 2000-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: McIninch, James TITLE OF INVENTION: PFILE REFERENCE: 38-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Boukharov, Andrey A. APPLICANT: Kovalic, David K. APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                           469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 LeuArg.....GluTyrGlnSerLysValLysArg 220
                                                                                                                                                                                                                                                                                                                                                                                                                                    61 rThrSerLeuSerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 GlyThrGlnThrGlyPheValArgTyrAsp.....AspGlyTyrValSe 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 .....AspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArg 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 gSerGlyGlyLeuMetProArgGlyHisAsnGluTyrPhe...... 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLysAr 18
                           yrArgValAsnPheGlyValIleAspGluArgLeuHisArgAsnArgGlu 144
                                                                                                                                 nGluValSerAlaLeuGlyGlyIleProTyrSerGlnIleTyrGlyTrpT 128
                                                                                             GCGCCTCCACCAGGTCGCCGGCCTC
                                                                                                                                                                                                                                      PheAsnValAsnAspValLeuGlyValTyrSerProHisProTyrGluGl 111
                                                                                                                                                                                                                                                                                                                                      erGlyTyrSerThrTyrTyrIleTyrValIleAlaThrAlaProAsnMet 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGCACCGTGATGGCGCTGGGCGAGCCGACGATCTTGACGGTGAACTCGC 429
                                                                                                                                                                                   .....CTTCCACATGCGGTCGTCGA 489
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1.103
44.615
.....GATCTCGAGGTGCGGCGGCGGCGGCG 553
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Percent Identity:
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                                                                                           .GAGGTCGGTGGG.... 526
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24.103
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APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: McIninch, James
FITLE OF INVENTION:
CURRENT APPT
CUPPT
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US-09-528-682-1 x US-09-620-392-59272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-620-392-59272
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; Sequence 59272, Applic
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CURRENT APPLICATION NUMBER: US/09/620,392

CURRENT FILING DATE: 2000-07-19

NUMBER OF SEQ ID NOS: 69652

SEQ ID NO 59272

LENGTH: 7657

TYPE: NA
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Percent Similarity:
                                                                5370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5145 GGTGTCAGGCTACGGAAGCAAGATTCCAAG......AAGAG 5179
                                                                                                                                            5369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              5180 AAGAAGAGGGTTGGGTGGCGGCGGCCATGGATACCTTGTAGGTGGCG 5229
111 nGluValSerAlaLeuGlyGlyIleProTyrSerGlnIleTyrGlyTrpT 128
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                                                                                                                                                                                                                                             rThrSerLeuSerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuS 78
                                                                                                                                                                                                                                                                                                                                    GlyThrGlnThrGlyPheValArgTyrAsp.....AspGlyTyrValSe 61
                                                                                                                                                                                                                                                                                                                                                                                                      .....AspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArg 46
                                                                                                                                                                               erGlyTyrSerThrTyrTyrIleTyrValIleAlaThrAlaProAsnMet 94
                                                                                                                                                                                                                                                                                                 GGGCACCGTGATGGCGCTGGGCGAGCCGACGATCTTGACGGTGAACTCGC 5329
                                                                                                                                                                                                                                                                                                                                                                                  ACCCAGATGTCGCCGTCAGTCAGCACCTGGCGGACGCGGACCATGCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gSerGlyGlyLeuMetProArgGlyHisAsnGluTyrPhe.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    luProTrpIleHisHis......AlaProGln 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGATGTTGTACTGGTGGCCGTTCCCCCACACCACCACGCC.....GAGG 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pGlyTyrArgLeuAlaGlyPheProProAspHisGlnAlaTrpArgGluG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACCGAGACCCGCCGTATGCGGCCGGAGACGACGTCGCCGCCGTCCCACC 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrArgAsp...ArgTyrTyrArgAsnLeuAsnIleAlaProAlaGluAs 160
                                                                                                 PheAsnValAsnAspValLeuGlyValTyrSerProHisProTyrGluGl 111
                                                                                                                                  5369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09620392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.00
1.103
44.615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent
                                                           .....CTTCCACATGCGGTCGTCGA 5389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1 to: 7657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.103
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                                                                                                                                                                                                                                                                                                                                                                                  5279
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alignment_block:
US-09-528-682-1 x US-09-514-000-219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Agrobacterium tumefaciens
US-09-514-000-219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/pna/US095A_COMB.seq:US-09-514-000-219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-09-514-000-219 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)B
CURRENT APPLICATION NUMBER: US/09/514,000
CURRENT FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 15034
SEQ ID NO 219
LENGTH: 11719
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 219, Application US/09514000
                                                                                                                                                                                                                                                                                                             6229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6153 CCTTCAGGGCGGTCTTTCAGCGCCGGGGGGGGGGGAAAT......A 6190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6103 AACGGGCAAAACCTTCATCCGCACGCTTCCAGCGCGCCAGGCTTTCCCAG 6152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5548 CGCCACCGCCCATCGACGGGTCCCCGCACCACGC 5582
                                                                                    6302 GAGAATCTTGATGCGCGCCTTGTATTTGTTGTCGCGGCGGCCGTGCAGGT 6351
                                                                                                                                                                                                                                                                                                                                                                                                                         6191 GCCGGTGATGGCGGCAATATCGGCATC...........CGGCAGCTTCA 6228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5454 CACCGAGACCCGCCGTATGCGGCCGGAGACGACGTCGCCGCCGCCGTCCCACC 5503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5390 GCGCCTCCACCAGGTCGCCGGCCTC.....GAGGTCGGTGGG.... 5426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 luProTrpIleHisHis......AlaProGln 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 Tyrargasp...argTyrTyrargasnLeuasnIlealaProalaGluas 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128
                                                                                                                                                                                                                                                                                                                                                                     49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 rg.GlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThrGl 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy 17
tPheAsnValAsnAspValLeuGlyValTyrSerProHisProTyrGluG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pGlyTyrArgLeuAlaGlyPheProProAspHisGlnAlaTrpArgGluG 177
                                                                                                                                                                                                 AATTCAACCTCGACCTGGCGGGCCAGTTCTTCTGCGCCGGTTTCATGTAC 6301
                                                                                                                                                                                                                                                                                                                                                               nThrGlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGATGTTGTACTGGTGGCCGTTCCCCCACACCACCACGCC.....GAGG 5547
                                                                                                                                                                                                                                                   euArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyTyr..... 80
                                                                                                                                                                                                                                                                                                             ATTCGGTGTTTTCAG.....CTCCGCG 6251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yrArgValAsnPheGlyValIleAspGluArgLeuHisArgAsnArgGlu 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....GATCTCGAGGTGCGGCGGCGGCGGCGGCG
                                                                                                                                   .....SerThrTyrTyrIleTyrValIleAlaThrAlaProAsnMe 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
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0.768
50.813
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12
22.358
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6352	TATAAACGCGCATGACGGCCGTGGTATAGGACAGCAGGTCCTCTTCCGGC	6401
111		121
6402		6451
122	TyrGlyTrpTyrArgVa	130
6452	GCCGACGTAAACGGCAAAACCGATCTCACCCTTGTCGTTCTTTTTCAGAT	6501
130		147
6502	GCAGGCCGATATCGTGGACCTGAATGGCGGCGCGCGCTCG	6545
147		163
6546	GCACCCGTCACCGCGATCTTGAACTTGCGCGCGCAGGAACGAGAATTCCGG	6595
164	LeuAlaGlyPheProProAspHisGlnAlaTrpArgGluGl 1	177
6596		6645
177		194
6646	CGACTTCGTCTGCGGCAGCACCCGCGAAATGA	6677
194		210
6678	TCGGCGGTCACGTTGCGAATGCAGTTACCCGACGTCTGCAGTGCGTGC	6727
211		
6728	TTCCACGCTTGCCAGTTCAGAGAGGATATCCGGCGT 6763	

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/cgn2_6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database sequences: 1014543
Database length: 727792371
Search time (sec): 403.9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search information block: Query: US-09-528-682-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Date: Jun 18, 2002 9:48
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-(a/cgn2_1/USPTO_spool/US09528682/runat_18062002_082444_7900/app_query.fasta_1.689
-(a/cgn2_1/USPTO_spool/US09528682/runat_18062002_082444_7900/app_query.fasta_1.689
-DB=Pendling_Patents_NA_Lwew -QFMT=fastap -SUFFIX=p2n.rnpn
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -GAPEXT=4.000 -GAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -FGAPOP=6.000 -FGAPOXT=7.000 -YGAPOD=10.000
-YGAPEXT=0.500 -DELCOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=DLOSum62 -TRANS=human40.cdi -LIST=1000 -DOCALIGN=20
-THR_SCORE=pCt -THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTPMT=pfs -NOBM=St -NEARSIZE=500 -MINLEN=0 -MAXIEN=200000000
-USER=US09528682_@CGN1_1_572 -NCPU=6 -ICPU=3 -LONGIGG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                   n2_6/ptcdata/1/pna/USS0_NEW_COMB.seq:US-09-919-002-8511 - 84.
n2_6/ptcdata/1/pna/USS0_NEW_COMB.seq:US-09-919-002-8517 + 83.
n2_6/ptcdata/1/pna/USS0_NEW_COMB.seq:US-09-919-002-8517 + 83.
n2_6/ptcdata/1/pna/USS0_NEW_COMB.seq:US-09-360-039-32681 + 83.
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n2_6/ptcdata/1/pna/USS0_NEW_COMB.seq:US-60-360-039-28417 + 81.
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n2_6/ptcdata/1/pna/USS10_NEW_COMB.seq:US-10-109-551-9 + 80.00.
n2_6/ptcdata/1/pna/USS10_NEW_COMB.seq:US-10-109-551-7 + 80.00.
n2_6/ptcdata/1/pna/USS10_NEW_COMB.seq:US-10-109-551-7 + 79.00.
n2_6/ptcdata/1/pna/USS10_NEW_COMB.seq:US-10-300-039-41301 - 79.00.
n2_6/ptcdata/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US99_NEW_COMB.seq:U.6/ptodata/1/pna/US99_NEW_COMB.seq:U.6/ptodata/1/pna/US90_NEW_COMB.seq:U.6/ptodata/1/pna/US10_NEW_COMB.seq:U.6/ptodata/1/pna/US10_NEW_COMB.seq:U.6/ptodata/1/pna/US10_NEW_COMB.seq:U.6/ptodata/1/pna/US09_NEW_COMB.seq:U.6/ptodata/1/pna/US09_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.seq:U.6/ptodata/1/pna/US60_NEW_COMB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pending_Patents_NA_New:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403.930000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq:US-09-919-002-6157 + 83.00 153.66 seq:US-09-919-002-6157 + 82.50 148.00 153.66 seq:US-09-919-002-6157 + 82.50 148.01 164.00 153.66 seq:US-09-919-002-6157 + 82.50 148.01 180 seq:US-60-360-039-33252 + 82.50 138.06 seq:US-09-540-2098-1507 + 82.50 138.06 seq:US-09-540-2098-2633 + 82.00 151.23 seq:US-60-360-039-31176 + 81.50 139.90 seq:US-60-360-039-31176 + 81.50 139.90 seq:US-60-360-039-31176 + 81.50 139.90 seq:US-60-360-039-31176 + 81.00 137.92 seq:US-60-360-039-31176 + 81.00 137.92 seq:US-60-360-039-31176 + 81.00 137.92 seq:US-10-109-551-1 + 80.00 145.71 5.92 seq:US-10-109-551-9 + 80.00 143.85 6.92 seq:US-10-109-551-9 + 80.00 143.85 6.92 seq:US-10-109-551-9 + 80.00 133.93 29.92 seq:US-10-109-51-9 + 80.00 133.93 29.
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11. Pina/US10_NEW_COMB. seq: US-1
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ptodata,
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alignment_block:
US-09-528-682-1
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; Sequence 1, Application US/09809033A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-128-714-6307 + /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-14978 /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-132329 + /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-32742 - /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-32742 - /cgn2_6/ptodata/1/pna/US90_NEW_COMB.seq:US-09-704-302A-280 + /cgn2_6/ptodata/1/pna/US90_NEW_COMB.seq:US-09-519-002-11904 - /cgn2_6/ptodata/1/pna/US90_NEW_COMB.seq:US-09-919-002-11904 - /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-41713 + /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-43715 + /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-37252 + /cg
                                                                                                                                                                                                                                                                                                                               ; SEQUENCE DESCRIPTION: US-09-809-033A-1
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Percent Similarity:
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                                                   Align seg 1/1
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REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: MCC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703,425-8405
TELEFAX: 703,425-8406
INFORMATION FOR SEQ ID NO: 1:
AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2022 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/809,033A
FILING DATE: 16-Mar-2001
CLASSIFICATION: <Unknown>
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Hendricks and Assoc
                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown MOLECULE TYPE: DNA (ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                          Quality: 1053.00
Ratio: 4.701
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: VA
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                                                   to: US-09-809-033A-1
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INVENTION: Chimeric Nontoxic Mutants
Enterotoxins as Mucosal Adminity
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; Sequence 2, Applicatio;
; GENERAL INFORMATION:
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  NUMBER OF
                                                                          TITLE
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SEQUENCES:
                                                                                                                                             Kiyono,
Takeda,
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151 ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPh 167
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                                                                                                                                                                         Application US/09809033A
                                   Yamamoto, Shingo INVENTION: Chimeric Nontoxic Mutants
                                                                            Ohmura, Mari
                                                                                            Hiroshi
Yoshifumi
                                                                                                                                    Jerry
Humoral Immunity
                  Enterotoxins as Mucosal
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                  Adjuvants for Cell-Mediated or
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alignment_block:
us-09-528-682-1 x us-09-809-033A-2
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Percent Similarity:
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 871
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COMPUTER: IBM PCFF0
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.
CURRENT APPLICATION DATE:
APPLICATION DATE: 16-Mar-2001
FILING DATE: 16-Mar-2001
CLASSIFICATION: CUNKnown>
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DCCKET NUMBER: MCG-01
TELECHONE: 703/425-8406
TELECHONE: 703/425-8406
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                                                          AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy
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MEDIUM TYPE: Floppy disk
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SEQUENCE DESCRIPTION:
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LENGTH: 2022 base pairs
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Ratio: 4.683
milarity: 93.333
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CITY: Fairfax
STATE: VA
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APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory S.
APPLICANT: Hinkle, Gregory C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT TILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 35377
LENGTH: 1653
TYPE: DNA
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; Sequence 35377, Application
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Agrobacterium tumefaciens US-60-360-039-35377
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                                                                                                                                                                 Align seg 1/1 to reverse of: US-60-360-039-35377
                                                                                                                                                                                                          US-09-528-682-1 x US-60-360-039-35377/rev
                                                                                                                                                                                                                                                                       Percent Similarity:
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                   1 AsnGlyAspArgLeuTyrArgAlaAspSerArgProProAspGluIleLy 17
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                                                                                                                                                                                                                                                                                                                                                             Sequence 38194, Application US/60360039 GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
                                                    SEQ ID NO 38194
LENGTH: 1653
                                                                                                  APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
ORGANISM: Agrobacterium tumefaciens
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US-09-528-682-1 x US-60-360-039-38194/rev
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                          336 TTCCACGCTTGCCAGTTCAGAGAGGATATCCGGCGT
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APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PRILE REFERENCE: 38-10(52052)A

CURRENT APPLICATION NUMBER: US/60/360,039

CURRENT APPLICATION NUMBER: US/60/360,039

CURRENT FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 38598

LENGTH: 1653

TYPE: DN*
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US-09-528-682-1 x US-60-360-039-38598/rev
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Quality:
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                                   lAsnPheGlyValIleAspGluArgLeuHisArgAsnArgGluTyrArgA 147
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                                                                                                                                                                                               lnGluValSerAlaLeuGlyGly......IleProTyr 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTCGGTGTTTTCAG.....CTCCGCG 813
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                                                                              GCCGACGTAAACGGCAAAACCGATCTCACCCTTGTCGTTCTTTTCAGAT 563
                                                                                                                 SerGlnIleTyrGly.....
                                                                                                                                                        AGGAAGTCGCGAATCTTCTTGGCGATCATCGGCGTACGGCCCTGCCCGCC 613
                                                                                                                                                                                                                                                                                                                                                          .....SerThrTyrTyrIleTyrValIleAlaThrAlaProAsnMe 94
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Percent Identity:
.CTGAATGGCGGCGCGCTCGCGCTCG 519
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seq_documentation_block:
; Sequence 37962, Application US/60360039
; GENERAL INFORMATION:
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Quality:
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SEQ ID NO 37962
LENGTH: 1657
TYPE: DNA
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
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                                                                                                                                                                                                                      873 GGCGGTGATGGCGGCAATATCGGCATC
                                                                                                                                                                                                                                                                                                                                 911 CCTTCAGGGCGGTCTTTCAGCGCCGGGGGGGGGAAAT...... 874
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812 AATTCAACCTCGACCTGGCGGGCCAGTTCTTCTGCGCCGGTTTCATGTAC 763
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                                                                                                                                                                                                                                                                                                                                                                                     17 sargSerGlyGlyLeu...MetProargGlyHisAsnGluTyrPheAspA 33
                                                                                                                                                                                                                                                                          33 rg.GlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThrGl 49
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                                                 euArgSerAlaH1sLeuAlaGlyGlnSerIleLeuSerGlyTyr.....
                                                                                                                                                               nThrGlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSerL
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Percent Identity:
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alignment_block:
US-09-528-682-1 x US-60-360-039-41495
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                                                                                                                                                                                                                                                                  US-60-360-039-41495
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                                                                                                                  Ratio:
Percent Similarity:
Align seg 1/1 to: US-60-360-039-41495
                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 41495
LENGTH: 2625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
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                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: SPHINGOMONAS
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                                                                                                                                                                 Quality:
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Percent Identity:
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seq_documentation_block:
    Sequence 4736, Applica
US-09-540-209B-4736
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                                                                                                                                               GENERAL INFORMATION:
APPLICANT: GATY L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
                     NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 4736
LENGTH: 3360
TYPE: DNA
ORGANISM: B.fragilis
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BACTEROIDES

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alignment_block:
US-09-528-682-1 x US-09-540-209B-4736
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Percent Similarity:
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                                            1991 AAAATACCCGTACCTGGCTGGATAACCTGAAAGTCCGTGCATCCTGGGGT 2040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..TATCAGGAATTCTATAAGAATTACTATACTGTAGATGCCGCAAAGAAA 1746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rProHisProTyrGluGln.....GluValSerAlaLeuGlyGlyIleP 120
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AspThrCysAsnGluGluThrGlnAsnLeuSerThrIleTyrLeuArgGl 213
                                                                                                                                           CTTCCCTTCCTTATCAGGTGCATGGCGCATCTCAGAAGAAGCTTCATGG 1990
                                                                                                                                                                                       yPheProProAspHisGlnAlaTrpArg.....GluGluProTrpIleH 181
                                                                                                                                                                                                                                                                                                                                   GCGTGAACTATGCATATAATTCCCCGGTATTTATTTGAGGCAAATTTC... 1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaThrAlaProAsnMetPheAsnValAsnAspValLeuGlyValTyrSe 105
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                                                                                         isHisAlaProGlnGlyCysGlyAsn...SerSerArgThrIleThrGly 196
                                                                                                                                                                                                                                       ...CGTTATGACGGCTCCTCACGTTTCCACAAAGATCATCGTTGGGGATT 1940
                                                                                                                                                                                                                                                                              ProAlaGluAspGly......TyrArgLeuAlaGl 166
                                                                                                                                                                                                                                                                                                                                                                               .....AsnArgGluTyrArgAspArgTyrTyrArgAsnLeuAsnIleAla 156
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGTACCAAAGGTGCAACCCAGGATTATGCCACACGTTCTGTATTTGGAC 1846
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APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 2852
LENGTH: 3027
TYPE: DNA
ORGANISM: B.fragilis
US-09-540-209B-2852
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US-09-528-682-1 x US-09-540-209B-2852
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Percent Similarity:
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                                                                    1699 ..TATCAGGAATTCTATAAGAATTACTATACTGTAGATGCCGCAAAGAAA 1746
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133 GlyValIleAspGluArgLeuHisArg......
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                                                                                                                                                                              ....CATACATTTGCTCAGAAACACGATGTATCCGCGCTGTTAGGC.... 1698
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                                                                                                                roTyrSerGlnIleTyr...GlyTrpTyrArgValAsnPhe...... 132
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Percent Identity:
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APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 46582
LENGTH: 1272
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                                             181 isHisAlaProGlnGlyCysGlyAsn...SerSerArgThrIleThrGly 196
49 GlnThrGlyPheValArgTyrAspAspGlyTyrValSerThrSerLeuSe
                                                                                               32 spArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaArgGlyThr 48
                                                                                                                                               69 AGACCTTCTGGGCTACGATGACTATGTTTATGAAGTTCTCGCAAACCCGG 118
                                                                                                                                                                                                                                                 19 CAGCCCACGGACCCTCTTGAGGAGGCTCGCGCGCAGCTCAGGAGAGCTGT
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                                                                                                                                                                                              Quality:
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0.956
48.128
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PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 43
LENGTH: 2338
TYPE: DNA
                                                                                                                                                                                                                                         alignment_block:
us-09-528-682-1 x us-10-104-047-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens US-10-104-047-43
                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                              Align seg 1/1 to: US-10-104-047-43
                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 43, Application US/10104047 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 isGlnAlaTrp 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391
  184 GGCAGCCCTGGAGGCAACCGCTACCCACCTCAGGGCGGGTGGTGGCTGGGG
                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                  86.00
0.827
52.261
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seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-104-047-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: Novel full length FILE REFERENCE: H1-A0105
                                                                                                                     134 GCCCGAAGCCTGGAGGATGGAACACTGGGGGCAGCCGATACCCGGGGCAG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 GGACATTCCCGCGCCCGACGTCTACACG......GATCCCCAGG 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 .IleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProProAspH 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 CTAAGATACTCTCCCCCAGGGAGCTTGAACTCCTGTCTAGG...... 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 heGlyValIleAspGluArg.....LeuHisArgAsnArgGlu 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 CCTCGCCGGCCTGCCTTATGGGGGAGGTAAGGGGGGGTGTTAGGGTTAACC 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 aLeuGlyGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 GGTACCAC.....ACTATGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 CTGGAGGAGCCAGCACAATAGCGCGCTAGGCCCCTACAAAGGCGGTGTTA 232
                                                     61 rThrSerLeuSerLeuArgSerAlaHisLeu.....AlaGlyG 74
                                                                                                                                                                             45 AlaArgGlyThrGlnThrGlyPheValArgTyrAspAspGlyTyrValSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 AspValLeuGlyValTyrSerProHisProTyrGluGlnGluValSerAl 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 hrTyrTyrIleTyrValIleAlaThrAlaProAsnMetPheAsnValAsn 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 rLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyTyrSerT
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seq_documentation_block:
    Sequence 257380, Application US/10027632
    SEREAL INFORMATION:
    APPLICANT: Wang, David G.
    TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
    TITLE OF INVENTION: Polymorphisms in the Human Genome
    FILE REFERENCE: 108827.129
; ORGANISM: Human US-10-027-632-252780
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PRIOR FILLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILLING DATE: 2000-02-24
PRIOR FILLING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILLING DATE: 1999-09-28
PRIOR FILLING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILLING DATE: 1999-08-09
PRIOR FILLING DATE: 1999-08-09
                                                                                                   NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FBSTSEQ for Windows Version 4.0
SEQ ID NO 252780
LENGTH: 2298
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 alLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyr 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 nIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProProAspH 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTACAGC...AACCAGAACAACTTTGTGCAC.........GACTGC
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alignment_block:
us-09-528-682-1 x us-10-027-632-252780/rev
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seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-919-002-8511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: US-10-027-632-252780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 ...HisAlaProGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAs 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 laLeuGlyGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsn 131
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                                                                                                                                                                                                                                         483 AGCTGTATTGTTTAAACGAGGGAGAGAACTTCAGC...CTGTGCTGCAGA
                                                                                                                                                                                                                                                                                                                                      574 GTCCACACA.....TGCACAAATTGTTCAAAGACAACAACCAAAGA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 laGlyPheProProAspHisGlnAlaTrpArgGluGluProTrpIleHis 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          884 CTCTCTCTCTCCTCCTCTTTGGTCAGCTTGTAGCTTTGAGGTACC 835
                                                                                                                                                                                        213 GluTyrGlnSerLysValLysArgGlnIlePheSerAspTyrGlnSerGl 229
                                                 386 GGTCAAATTGTAT 374
                                                                                          229 uValAspIleTyr 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 nAspValLeuGlyValTyrSerProHisProTyrGluGlnGluValSerA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 uSerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGlyTyrS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 GlyPheValArgTyrAspAspGlyTyrValSerThr.....SerLe
                                                                                                                                              GGAGGAAAGACAGCAGTAAACAAAGAGGACTATGATAGGCTAGTGTTACA
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                                                                                                                                                                                                                                                                                  .......CysAsnGluGluThrGlnAsnLeuSerThrIleTyrLeuArg 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....TGGAGAGAACACACATACATGCAC
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Gaps:
Percent Identity:
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seq_documentation_block:
; Sequence 8511, Application US/09919002
; GENERAL INFORMATION:

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CURRENT APPLICATION NUMBER: US/09/919,002
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09,
PRIOR FILING DATE: FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US
PRIOR FILING DATE: FILING DATE: 1998-02-13
NUMBER OF SQ ID NOS: 13203
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 8511
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US-09-528-682-1 x US-09-919-002-8511/rev
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TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-752CON1
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APPLICANT: Liu, Jin
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191
                                                                                                                                  181 sHisAlaProGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspT 198
                                                                                                                                                                                                                                                                                                                            150 yrArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArg.....Leu
                                                                                                                                                                                                                                                                                                                                                                                   379
                                                                                                                                                                                                                                                                                                                                                                                                                 134 llleAspGluArgLeu...HisArgAsnArgGluTyrArgAspArgTyrT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             429 ACTATCGCTTGTCACAAGACACAGACAATCAGACCAAAAGTATTTGCTGT
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                                          198 hr 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   652 GTTCGGTTTGATGGCGTGTATATCAGTAAAACCACATATATTCGTCAA.. 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lSerAlaLeu...Gly.GlyIleProTyrSerGlnIleTyrGlyTrpTyr 128
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CT 190
                                                                                                                                                                                       CAGCTATGTTCCAGTGGTCACCAGAGGTTCAACAAACTCATCTGGATACA
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                                                                                       TCATTCT.
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alignment_scores:
    Quality:
    Ratio:
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US-09-528-682-1 x US-09-919-002-6157
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APPLICANT: Leshkowitz, Dena
APPLICANT: Liu, Jin
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SEQ ID NO 6157
LENGTH: 3617
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CURRENT APPLICATION NUMBER: US/09/919,002
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922
PRIOR PILING DATE: FILING DATE: 1999-07-22
PRIOR FILING DATE: APPLICATION NUMBER: US 09/034,341
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,341
PRIOR FILING DATE: FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 13203
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                                                            2475 AACACAGGAGGATTCACACCGGAGAGAAACCCTACCAATGTGAAGAATGT 2524
                                                                                                                                                                                                                                                                                                                                                                                    2334 AACCTTTCAAATGTGAGGAATGTGACAGCATCTTCAAGTGGTTCTCAGAC
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                                                                                                                                                                        CAAATGTGACGAATGTGGGAAAGCCTATACACAGTCCTCACACCTCAGTG
                                                                                                                                                                                                                       sArgAsnArgGluTyrArgAspArgTyrTyrArgAsnLeuAsnIleAla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGlyGlyI 119
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                                                                                                              .....ProAlaGluAspGlyTyrArg.....
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.....LeuAlaGlyPheProProAspHi 171
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APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN ITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/50/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 4/374
SEQ ID NO 32681
LENGTH: 1107
TYPE: DNA
ORGANISM: Chloroflexus aurantiacus
US-60-360-039-32681
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; Sequence 32681, Applic
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Ratio:
Percent Similarity:
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                                                                                                                                          276
                                                                                                                                                                                                                            226 AGCANATCGTTCGGCGAACTGAACCGACTGTACGACTGGATGATCGAACA 275
                                                                                                                                                                                                                                                                                                                         191 G.....CGTTCACACGACCACTGTGCCATCAGGTGAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                    141 GACCGCCATTGCCGATCAGACCGCAGCCCACCTGACAGCAGCCGGGTATC
                                             326 GTGACCTGGCAGGGTTTGCGGCAGCGACCATC.........
71 LeuAlaGlyGlnSerIleLeuSerGlyTyrSerThrTyrTyrIleTyrVa 87
                                                                                                                                                                                                                                                                         29 luTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAla 45
                                                                                                                                                                                                                                                                                                                                                                  Arg.......GlyThrGln.ThrGlyPhevalA 54
                                                                                           rgTyrAspAspGlyTyrValSerThrSerLeuSerLeuArgSerAlaHis
                                                                                                                                        CGGAATCGAACGCCGTGATGTCGTCCTGGCCCTCGGTGGTGGCGTGGTCG
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Sequence 3223, Application US/60360039

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Blater Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT APPLICATION NUMBER: US/60/360,039
LENGTH: 1524
TYPE: DNO 32252
LENGTH: 1524
TYPE: DNA
OPERANTEN: Balternia motalitations
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US-09-528-682-1 x US-60-360-039-32252
                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
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                                                                                                                                                            Align seg 1/1 to: US-60-360-039-32252 from: 1
                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 508 CTGCTGGCGACACTACCGGCTCGCGAGCTACGCGCCGGCTGGGCCGAAGT
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                                                       415 GCGGACAGCGCTCCGATGGAAGACGCCTACCGTCACGGCGACGACCTGGC 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             608 CACTCGC......CGCAACCCAACGCTGGCACGCCGACAATCCG
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21 .GlyLeuMetProArgGlyHisAsnGluTyrPheAspArgGlyThrGlnM 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProTrpIleHisHisAlaProGlnGlyCysGlyAsnSerSerArgThrIl 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uTyrArgAspArgTyrTyrArgAsnLeuAsnIleAlaProAlaGluAspG
                                                                                                       AlaAspSerArgProProAspGluIleLysArgSerGly.....
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Percent Identity:
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                                                 CATCCGGCCGTCGCGCAGTCGTCTGTGATCGGTGT 1325
                                                                                                                                              GTGGCGAGAACGT...CTATTCCGCCGAGGTGGAGAAGGCGCTGGCGAGT
                                                                                                                                                                                                                                             GGACGGCTTCCTGGTCGTCGACCGCCTGAAGGACATGATCATCAGCG 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCCGAATGTGATGCTCGGCTACTGGAACCAGCCGCAGGCTACCGCGGAG 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uArg.LeuHisArgAsnArg.GluTyrArgAspArgTyrTyrArgAsnLe 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCTTGGCCCGGAGTATCACGACGCGGCGGCGCGCGAGCGGCAAGATG 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATCCAGATGGGG.....CTGGACTGGATGGACCGGCATCCGGGGGCGCG 793
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                                                                                            erSer.....ArgThrIleThrGlyAspThrCys 199
                                                                                                                                                                                           aTrpArgGluGluProTrpIleHisHisAlaProGlnGlyCysGlyAsnS 190
                                                                                                                                                                                                                                                                                                                                         GCGATCCGCAATGGCTGGATGCATACCGGCGACGGTGGGTACATGGACAA 1193
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/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-540-209B-1507
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CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 1507
LENGTH: 3000
TYPE: DNA
ORGANISM: B.fragilis
US-09-540-209B-1507
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Sequence 1507, Application US/09540209B
GENERAL INFORMATION:
APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
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US-09-528-682-1 x US-09-540-209B-1507
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                                                                                                                                                                                                                                                                        143 ArgGluTyrArgAspArgTyrTyrArgAsnLeuAsnIleAlaProAlaG1 159
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                                                                                                                                                                                                                                          GAAGAGATGCAATCC.....TATCAGAACGG......AA 895
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                                                              AATTACAAGTTGGCTCTTTCCAATGGTAGCGAGAAGACCCAATATTACAT
                                                                                                       spHisGlnAla.....Trp...ArgGluGluProTrpIleHis 181
                                                                                                                                                       CGGGGGGCATCGACTGGCAGGATGAGATTTTCCGTACGGGGATCACCCAG
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44.292
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Sequence 2633, Application US/09540209B

GENERAL INFORMATION:
APPLICANT: GATY L. Breton
ITITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRATITLE OF INVENTION: FOR DIACNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT ELING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 2633
TYPE: DNA
GRGANISM: B.fragilis
US-09-540-209B-2633
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US-09-528-682-1 x US-09-540-209B-2633
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                          sProTyrGluGlnGluValSerAla....
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                                                                                                                  aProAsnMetPheAsnValAsnAspValLeuGlyValTyrSerPro..Hi 107
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APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (UTILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 27746
LENGH: 3291
TYPE: DNA
ORGANISM: Neurospora crassa
US-60-360-039-27746
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US-09-528-682-1 x US-60-360-039-27746
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; Sequence 27746, Application US/60360039
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Percent Similarity:
                                                                                                                                                                 Align seg 1/1 to: US-60-360-039-27746
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                                                                    2017 GACATGGGCACGATCGACGGGCAGATTGCGACTCAGGTGTTAACACTAGC
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56 AspAspGlyTyrValSerThrSerLeuSerLeuArgSerAlaHisLeuAl 72
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APPLICANT: Cdo, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Stater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 28417
LENGTH: 2028
TYPE: Nw"
                                                                                                                                                                                                                                                                                                                            alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Burkholderia fungorum US-60-360-039-28417
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                                                                          TTTCCGCCAGATGGGCAGCAAGACACCGGGCCCACCCGGAGTACCGCATGA 352
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Percent Identity:
                           PheAspArgGlyThrGlnMet 37
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seq_documentation_block:
   Sequence 31176, Application US/60360039
   GENERAL INFORMATION:
   APPLICANT: Cao, Yongwei
   APPLICANT: Chen, Xianfeng
                                                                                                                                         seq_name: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-31176
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                                                                                                                                                                                                                                                                                AAAGGCGTTGCGTCACGCGAATCGTCGGGCAAG 1122
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 31176
SEQ ID NO 31176
US-60-360-039-31176
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US-09-528-682-1 x US-60-360-039-31176
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Percent Similarity:
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                          GCCCGATGCGCCGCTGTTCGACTATCGGGTCTACGCGTTGTGCGGCGACG
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AGCAGGACACCTCGGCGCGCGCACGGCGAGCCGCTCGGCGTAGAAGAAGTG 843
                                                                                 GCTGATCGTGCTGCACAGCATCATCGGCTGGGGGGGCGCCCCAT....A 793
                                                                                                                        nMetPheAsnValAsnAspValLeuGlyValTyrSerProHisProTyrG 110
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Gaps: 11
Percent Identity: 19.142
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; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 42281
; LENGTH: 2004
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US-09-528-682-1 x US-60-360-039-42281
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Percent Similarity:
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GENERAL INFORMATION:
APPLICANT: Cao, Yougwei
APPLICANT: Chen, Xianfeng
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518 GCTTCTCCGCG...
                                          127 rpTyrArgValAsnPheGlyValIleAspGluArgLeuHisArgAsnArg 143
                                                                                               468 GATGCTGGCGCGCGCGCCCCCGCGCGCACACTCGGTGGTGTTCGCGG 517
                                                                                                                                                                                          418 GACGACATCGTCACGCTGTACATGCCGATGGTGCCCGAGTTGCCGATCGC
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Percent Identity:
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alignment_block:
US-09-528-682-1 x US-10-105-299-12516/rev
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; ORGANISM: Homo sapiens
US-10-105-299-12516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-105-299-12516
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Percent Similarity:
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CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
Prior Application removed - See File Wrapper or Palm SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen, et. al TITLE OF INVENTION: Human Secreted Proteins FILE REFERENCE: PS950
                                                                                                                                                                                                                                                                                                                                                                                                   1663
                                                                                                                                                                                1566 AGAATTGGAAAAAACTACTTTAAAGTTCATATGGAACCAAAAAAAGAGCCC 1517
                                                                                                                                                                                                                                                                                            1616
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                                                                                 1516 ACATCGCCAAGGCAATCCTAAGCCAAAAGAACAAAGCTGGAGGCATCACA 1467
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                                                                                                                               69 aHisLeuAlaGly.....
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US-10-109-551-1
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                                        SOFTWARE: PatentIn V
SEQ ID NO 1
LENGTH: 78056
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10109551
GENERAL INFORMATION:
                                                                                                                                                                                                               APPLICANT: PIEDRAHITA, JORGE
TITLE OF INVENTION: TRANSGERIC ANIMALS RESISTANT
TITLE OF INVENTION: SPONGIFORM ENCEPHALOPATHIES
FILE REFERENCE: TAMK: 207US
CURRENT APPLICATION NUMBER: US/10/109,551
CURRENT FILING DATE: 2002-03-28
                                                                                                                                                                                                                                                                                                                                        APPLICANT: DUNNE, PATRICK W. APPLICANT: PIEDRAHITA, JORG
                                                                                                                                                                 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2001-03
                                                                                                                                             NUMBER OF SEQ ID NOS:
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seq_documentation_block:
Sequence 7, Application US/09831271A
GENERAL INFORMATION:
APPLICANT: RIESMEIER et al., Jorg
TITLE OF INVENTION: PROMOTERS FOR GENE EXPRESSION IN ROOTS
FILE REFERENCE: 0147-02259
CURRENT APPLICATION UMBER: US/09/831,271A
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 41
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US-09-528-682-1 x US-10-109-551-1
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US-09-528-682-1 x US-09-831-271A-7
                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (256)..(1197)
US-09-831-271A-7
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                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1 SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Lycopersicon esculentum
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to: US-09-831-271A-7
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 830
; TYPE: DNA
; ORGANISM: Cervus elaphus
US-10-109-551-9
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; Sequence 9, Application US/10109551
; GENERAL INFORMATION:
                                                                                                                                     alignment_block:
US-09-528-682-1 x US-10-109-551-9
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    Quality:
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                                                                                        Align seg 1/1 to:
                                                                                                                                                                                                             Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DUNNE, PATRICK W.
APPLICANT: DIEDRAHITA, JORGE
TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
TITLE OF INVENTION: SPONGIPORM ENCEPHALOPATHIES
FILE REFERENCE: TAMK:207US
CURRENT APPLICATION NUMBER: US/10/109,551
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/280,549
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 10
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                                          114 SerAlaLeuGlyGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgVa 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 spGluArgLeuHisArgAsnArgGluTyr...........Arg 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 ACCAACCACAGTAGTCAAAAGT......GAAGACTTCAAGGTACCCT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 eProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyValIleA 136
397 GCAGTGGTAGGGGGCCTC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    457 TTGACTACTTCAAGAAG 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 alaspileTyrasnarg 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uTyrGlnSerLysValLysArgGlnIlePheSerAspTyrGlnSerGluV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATAACTACAAGAAGGAGTCA..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAAGTATCATTTGTTCCCGAACATGAATCATTCCTGCCAAAGAATGACT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTACCCTCGAAGGCTAAACCAGAATATAAGGAGTCATTTTTTCAAAAT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspThrCysAsnGluGluThrGlnAsnLeuSerThrIleTyrLeuArgGl 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATGATTACTATAAGAAGCCATCAATT....TCAGAGGATAACTATAA 298
                                                                                           US-10-109-551-9
                                                                                                                                                                                                          80.00
1.194
54.032
                                                                                                                                                                                                             Gaps:
Percent Identity:
                                                                                           from:
GGTGGCTACTTGCT 428
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: 24.194
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alignment_scores:
Quality:
Ratio:
Percent Similarity:
                                                                                                                                  alignment_block:
US-09-528-682-1 x US-10-096-080-25
                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (60)..(824)
US-10-096-080-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-096-080-25
                                                                                     Align seg 1/1 to: US-10-096-080-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/128,450
PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/10096080 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chesebro, Bruce W
APPLICANT: Caughey, Byron W
APPLICANT: Chabry, Joelle
APPLICANT: Priola, Susette
TITLE OF INVENTION: Inhibitors of Formation of Protease Resistant Prion
TITLE OF INVENTION: Protein
FILE REFERENCE: 50121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/096,080 CURRENT FILING DATE: 2002-03-11 PRIOR APPLICATION NUMBER: US/09/823,494 PRIOR FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Hamster sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1000
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                     114 SerAlaLeuGlyGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgVa 130 ::::::::::::||||||| ::
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417 GCCGTGGTGGGGGGCCTT......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rGlnSerGluValAspIleTyr 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACATCAAGATGATGGAGCGAGTTGTGGAGCAAATGTGCATCACCCAGTA 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TyrLeuArgGluTyrGlnSerLysValLysArgGlnIlePheSerAspTy 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pIleHisHisAlaProGlnGlyCysGlyAsn.....SerSerArgT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgLeuAlaGlyPheProProAspHisGlnAlaTrpArgGluGluProTr 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spArgTyrTyrArg...AsnLeuAsnIleAlaProAlaGluAspGlyTyr 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGAGAGAATCCGAGGCTTAT 714
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Identity:
... GGTGGCTACATGCT 448
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24.194
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FILE REFERENCE: CLD01236

CURRENT APPLICATION NUMBER: US/10/144,781

CURRENT FILING DATE: 2002-05-15

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 41

LENGTH: 2701

TYPE: DNA

ORGANISM: Mus musculus

US-10-144-781-41
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    Sequence 41, Application US/10144781
    SEQUENCE INFORMATION:
    GENERAL INFORMATION: Gangadharan et al.
    APPLICANT: SUBRAMANIAN, Gangadharan et al.
    TITLE OF INVENTION: MOUSE ORTHOLOGS OF HUMAN DRUG TARGET
    TITLE OF INVENTION: GENES, PROTEINS ENCODED BY THESE MOUSE GENES, AND USES
    TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-528-682-1 x US-10-144-781-41/rev
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                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: US-10-144-781-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
Percent Similarity:
                                                                                                                                                                       2330 GCCCTATGCCGTAGCCCTCGATCGCAAAGGGTTTGCCCACGGTGAGCAGC 2281
                                                                                                                                                                                                                                                                                         2380 CCTACTGATGAACTCTGACAGGTTGGAGGTGAGCGGCGAATTTTGGGGCA 2331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           663 GACATCAAGATAATGGAGCGCGTGGTGGAGCAGATGTGTACCACCCAGTA 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 TyrLeuArgGluTyrGlnSerLysValLysArgGlnIlePheSerAspTy 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             622 CAGTCACCACCACCAAGGGGGAG..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         584 TGTGCAC.....GATTGTGTCAACATCACCATCAAGCAGCACA 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 lAsnPheGlyValIleAspGluArgLeuHisArgAsnArgGluTyrArgA 147
  46
                                                                                                                                                                                                                          12 ProProAspGluIleLysArgSerGlyGly......LeuMetProAr
                                                                                                              etAsnIleAsnLeuTyrAspHisAla..
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...ArgGlyThrGlnThrGlyPheValArgTyrAspAspGlyTyrValSe 61
                                                        TTGCAGTCCGCATCTATGGACACCTCATAATCCAGTAGTGATTTATCCAT 2231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGG......CCAGTGGACCAGTACAACAACCAGAACAACTT 583
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0.792
48.325
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Gaps:
Percent Identity:
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alignment_block:
US-09-528-682-1 x US-09-540-209B-2740
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; ORGANISM: B.fragilis
US-09-540-209B-2740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-540-209B-2740
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                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 2740
LENGTH: 3264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2740, Application US/09540209B
GENERAL INFORMATION:
APPLICANT: GRATY L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
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                                                                                 1558 TACAACGCAGATAACGAA...CCGTACCTGATTTCATGGAACGGCGGCGC 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 nGluValSerAlaLeuGlyGlyIleProTyrSerGlnIleTyrGlyTrpT 128
       22 uMetProArgGlyH1s...AsnGluTyrPheAspArgGlyThrGlnMetA 38 ::: :: :: |||||||||
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                                                                                                             TyrArgAlaAspSerArgProProAspGluIleLysArgSerGlyGlyLe 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erGlyTyrSerThrTyrTyrIleTyrValIleAlaThrAlaProAsnMet 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rThrSerLeuSerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....CAGCTCCTCAAATGTCTTGTCCCCGACCATGA 2001
                                                                                                                                                                                                                                                                                                                                              Quality:
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                                                                                                                                                                                                                                                                                                                        Ratio:
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0.748
48.858
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                                                                                                                                                                                                                                                                                               Percent Identity:
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19.635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 59, Application PC/TUS0209921 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: INCYTE GENOMICS, INC.
                                                                                                                                                       APPLICANT:
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                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1763 AAAAGAGCACACTGATTTCAAGTTCGGTGCCTACCATC........ 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 aLeuGlyGlyIleProTyrSerGlnIleTyrGlyTrpTyr...ArgValA 131
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LIU, Tommy ...
NGUYEN, Duy-Viet /
                                                                                                     AMSHEY, St.
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CHINN, Joyce
                                                                                                                                                                                                                                                                                                                                            TRAN, Alanna-Phung
                                                                                                                                                                                                                                                                                                                                                                  DAFFO, Abel
JONES, Anissa L.
                                                                                                                                                                             TUASON, Olivia
                                                                                                                                                                                                                                                  DUFOUR, Gerard E.
                                                                                                                                                                                                                                                                                                                        DAHL, Christopher
                                                                                                                                                    YAP, Pierre E.
                                                                            DAM, Tam C.
                                                                                                                                                                                                                          HILLMAN, Jennifer L.
                                                                                                                                                                                                   Jimmy
                                                                                                     Stefan R.
TY, Sean C.
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alignment_block:
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; OTHER INFORMATION: Incyte
PCT-US02-09921-59
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PRIOR FILING DATE: 2001-03-29; 2001-03-29; 2001-05-16; 2001-05-17; 2001-05-17; 2001-06-19; 2001-06-20; 2001-06-20
NUMBER OF SEQ ID NOS: 1146
SOFTWARE: PERL Program
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APPLICANT: URASHKA, Michael
TITLE OF INVENTION: SECRETORY MOLECULES
FILE REFERENCE: PT-1232 PCT
CURRENT APPLICATION NUMBER: PCT/US02/09921
CURRENT FILING DATE: 2002-03-27
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TYPE: DNA
ORGANISM: Homo sapiens
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GAAGTCCCTTCATTTGTCTCCTCAAGAACAATCT......GCCAGTT
                                   .ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyP 167
                                                                              CCTAAAAAAAGGGGGAAATTGTGATCTCAGCCACCAGGAAAGACTTCAGTC
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                                                                                                                                                          TGGAGATGAATCAAGGCGTTTCAGAGGAAAGAATTCACCTTGGCTCTAGC
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GERSTIN JR., Edward PERALTA, Careyna H.
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0.803
50.769
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Gaps:
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APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 26953
LENGTH: 769
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US-09-528-682-1 x US-60-360-039-26953
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    Quality:
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; ORGANISM: Neurospora crassa
US-60-360-039-26953
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Percent Similarity:
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TCTACTCCATGCGCAACGGGACCGACCTTTCCCCCTTCTGCCCTTGCCAAC
                                          euTyrAspHisAlaArgGlyThrGln..........ThrGly
                                                                                           GTTCCCATCGACAGTGCAGTTCGCCGAGTACACCCAAGCCAACGCCCAGC
                                                                                                                                                                                         GATATCGTGATGGCGCTTTTGAACCAAACCAAGTTAACCAACTGTTT 214
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0.731
40.449
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Gaps: 13
Percent Identity: 20.599
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alignment_block:
US-09-528-682-1 x US-10-109-551-7
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                                                                                                                                                                                                                                ; ORGANISM: Odocoileus hemionus hemionus US-10-109-551-7
                                                                                                                                                               alignment_scores
                                                                                                  Quality:
Ratio:
Percent Similarity:
Align seg 1/1
                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 771
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/10109551 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DUNNE, PATRICK W.
APPLICANT: PIEDRAHITA, JORGE
TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
TITLE OF INVENTION: SPONGIFORM ENCEPHALOPATHIES
FILE REFERENCE: TAMK:207US
CURRENT APPLICATION NUMBER: US/10/109,551
CCURRENT FILING DATE: 2002-03-28
CCURRENT FILING DATE: 2002-03-28
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/280,549
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTCTCGACAAGCACCACCCAGACATCACCCTCCACCAGGGTATCAA 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTTGCGTCGTTGGCGAAGGTCCCCTATGCCGCCCACGGCTACGCACAGT 480
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  to: US-10-109-551-7
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54.032
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6
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; SEQ ID NO 5
; LENGTH: 830
; TYPE: DNA
; ORGANISM: Odocoileus virginianus
US-10-109-551-5
                                                                                                                                                                                                                                   alignment_block:
US-09-528-682-1 x US-10-109-551-5
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                                                                                                                                                                                                                                                                                                               Percent Similarity:
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APPLICANT: DUNNE, PATRICK W.
APPLICANT: DIEDRAHITA, JORGE
APPLICANT: PIEDRAHITA, JORGE
TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT
TITLE OF INVENTION: SPONGIFORM ENCEPHALOPATHIES
FILE REFERENCE: TAMK: 207US
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CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/280,549
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399
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                                        130 lAsnPheGlyValIleAspGluArgLeuHisArgAsnArgGluTyrArgA 147
                                                                                                                    114 SerAlaLeuGlyGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgVa 130 ::::::::::::||||||| ::
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                                                                                           397 GCAGTGGTAGGGGGCCTT......GGTGGCTACATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    613 GACATCAAGATGATGGAGCGAGTTGTGGAGCAAATGTGCATCACCCAGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  534 TGTGCAT.....GACTGTGTCAACATCACAGTCAAGCAACACA
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429 GGGAAGTGCCATGAGCAGACCTCTTATACATTTTGGCAATGACTATGAGG
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                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
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1.179
54.032
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Gaps:
Percent Identity:
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alignment_block:
US-09-528-682-1 x US-10-106-698-580/rev
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    Quality:
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION UMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
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PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
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PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
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                                                                          855 ACACAGGGGTGTGACCAGCACTCCCCCTGCTACCTGCCGTGTGGGCAGGG 806
                                                                                                                                                 108
                                                                                                                                                                                                                    905 GCTCCTCGGAATCTATTCCAGTAGATTCTTTGCCGAGGGCATCACATATC 856
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                                                                                                                                                                                                                                                                                                                                                              955 TTTTTTTTTTTTTTTTTGCTGGAAACCAACATTTATTGAGCACTCCT 906
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GlyGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGl 133
                                                                                                                                                                                                                                                                                       pValLeuGlyValTyrSerProHis.....
                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrTyrIleTyrValIleAlaThrAlaProAsnMetPheAsnValAsnAs 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rGlnSerGluValAspIleTyr 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACATTAAGATGATGGAGCGAGTTGTGGAGCAAATGTGCATCACCCAGTA 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyrLeuArgGluTyrGlnSerLysValLysArgGlnIlePheSerAspTy 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pIleHisHisAlaProGlnGlyCysGlyAsn.....SerSerArgT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGAGAGAATCCCAGGCTTAT 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGTCACCACCACCAAGGGGGAG.....AACTTCACCGAAACT 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgLeuAlaGlyPheProProAspHisGlnAlaTrpArgGluGluProTr 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to reverse of: US-10-106-698-580
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Percent Identity: 19.663
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Quality:
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; Sequence 12700, Applic
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CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
Prior Application removed - See File Wrapper Software: Patentin Ver. 2.0
SEQ ID NO 12700
LENGTH: 6078
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TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
FILE TOTAL 
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seq_documentation_block:
; Sequence 41301, Application US/60360039
; GENERAL INFORMATION:
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APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
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CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 41301
LENGTH: 1050
TYPE: DNA
ORGANISM: Xylella fastidiosa
US-60-360-039-41301
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US-09-528-682-1 x US-60-360-039-41301
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AATCAACGACGCCTATGAGCGCATGCTC 996
                                     uTyrArgAspArgTyrTyrArgAsnLeu 153
                                                                                    TGCGCGGAGCACATCGTCGCGGACATCGAGCTGATCCGCGCAGAGGA
                                                                                                                     ArgValAsnPheGlyValIle...AspGluArgLeuHisArgAsnArgGl 144
                                                                                                                                                                                                          .....SerAlaLeuGlyGlyIleProTyrSerGlnIleTyrGlyTrpTyr 128
                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTGAACACGGTGGCCGCGCCGCACGACCTCAACGCCTTCATGACGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                leTyrValIleAlaThrAlaProAsnMetPheAsn......
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Gaps:
Percent Identity:
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seq_name: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-24895

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alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
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APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Methanobacterium thermoautotrophicum
US-60-360-039-24895
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; Sequence 24895, Application US/60360039
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-528-682-1 x US-60-360-039-24895/rev
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LENGTH: 1272
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233 yrAsnArgIleArgAspGluLeu 240
                                                                                       216 rLysValLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleT
                                                                                                                                                                                                                                                                        183 laProGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCys 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 laGluAspGlyTyrArgLeuAlaGlyPheProProAspHisGlnAlaTrp 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 gAsnArgGluTyrArgAspArgTyrTyrArgAsnLeuAsnIleAlaProA 158
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                                            TGAAGCTACGCGCCGGTTCATAGCCACCTATGAGTTCTATGACGATGTCT
                                                                                                                                      CTTGTTGGCTGTTACAACATGTTTACCATTTTCTAT...GGCCTTCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyTrpTyrArgValAsnPhe...GlyValIleAspGluArgLeuHisAr 141
                                                                                                                                                                              AsnGluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSe 216
                                                                                                                                                                                                                           TCCCAGTGCCTTGC......AAGGAGTGC
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Percent Identity:
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APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)A
CUBRENT APPLICATION NUMBER: US/60/360,039
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 34717
LENGTH: 1299
TYPE: DNA
ORGANISM: Ferroplasma acidarmanus
US-60-350-039-34717
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APPLICANT: Chen, Xianf
APPLICANT: Goldman, Ba
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                                                                                                                                                                                       583 AGCATTGAAAAGCTGTTCAAAGAACACAGGAATGAAATTGCTGCGGTAAT 632
                                                                                                                                                                                                                                                                                                                                                                                483 ATCCGGCAGTGGCACCATGACATTCGGAGTTCCATCTTCTGCAGGTGTAC
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                                                                                                                                                                                                                                                                                                                             92 roAsnMetPheAsnValAsnAspValLeuGlyValTyrSerProHisPro 108
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CGGAGAATGATTTTTGAACTCTCTACGGGAAATAACTGAGAAATATTCA
                                                                                            TACAGAACCGGTTCTTGGA.....AATATCGGTGTTATAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....CACGGTGCACATGACTATGCCCTGATAAA 482
                                         .....AspGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyr 150
                                                                                                                                                                                                                                                                                      CGGAGGAAGTTTCCAGAACAGTGCTTGTTGGGAGATACAATGACGCTGAA
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151 ArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArg......

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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 10887.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-07-2
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-01-28
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/166,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-08-09
PRIOR FILING DATE: 1999-09-08-09
PRIOR FILING DATE: 1999-09-08-09
PRIOR FILING DATE: 1999-09-08-09
                                                                                                                                alignment_block:
US-09-528-682-1 x US-10-027-632-138411
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Quality:
Ratio:
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   Sequence 138411, Application US/10027632
   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Human US-10-027-632-138411
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                                                                               Align seg 1/1 to: US-10-027-632-138411
                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 138411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCCTGCTCATATTTGATGAAGTAATAACCGGCTTTAGATTCGGATTTAA 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    euArgGluTyrGlnSerLysValLysArgGlnIlePheSerAspTyrGln 227
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Percent Identity:
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alignment_block:
US-09-528-682-1 x US-10-027-632-138412
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    Sequence 138412, Application US/10027632
    GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PELLORIUN NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1099-11-23
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-10-027-632-138412
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SEQ ID NO 138412
LENGTH: 806
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                     136
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                                                                                                                                                                                                                                             103 lTyrSerProHisProTyrGluGlnGluValSerAlaLeuGlyGlyIleP 120 : ||| ||| :::|||||| ::: |||||||
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                                 pGluArgLeuHisArgAsnArgGluTyr 145
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seq_documentation_block:
   Sequence 227, Application US/09602777A
   GENERAL INFORMATION:
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US-09+528-682-1 x US-10-109-551-3
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Quality:
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; Sequence 3, Applicatio
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                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-602-777A-227
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CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/280,549
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APPLICANT: PIEDRAHITA, JORGE
TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
TITLE OF INVENTION: SPONGIFORM ENCEPHALOPATHIES
APPLICANT: Pompejus, Markus APPLICANT: Kroger, Burkhard
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NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 SerAlaLeuGlyGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgVa 130
                                                                                                                                                                                                                                                                      226 rGlnSerGluValAspIleTyr 233
                                                                                                                                                                                                                      CCAGAGAGAATCCCAGGCTTAT 22961
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                                                                                                                                                                                                                                                                                                                                                                               TyrLeuArgGluTyrGlnSerLysValLysArgGlnIlePheSerAspTy 226
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; NAME/KEY: CDS
; LCCATION: (101)..(997)
; OTHER INFORMATION: RXA01932
US-09-602-777A-227
                                                                                                                                          SEQ ID NO 227
LENGTH: 1020
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PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932127.2
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TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
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                                                                                 FEATURE:
                                                                                                  ORGANISM: Corynebacterium glutamicum
                                                                                                                         TYPE: DNA
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APPLICATION NUMBER: DE 19932129.9
FILING DATE: 1999-07-19
APPLICATION NUMBER: DE 19932226.0
FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: DE FILING DATE: 1999-08-3
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APPLICATION NUMBER: DE 19932928.1
FILING DATE: 1999-07-14
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APPLICATION NUMBER: DE 19932128.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: DE 19933002.6 FILING DATE: 1999-07-14
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Zelder, Oskar
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alignment_scores:

Quality: Ratio:

Length: Gaps:

862

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| NUMBER OF SEQ ID NOS: 10444
| SEQ ID NO 1521
| LENGTH: 1293
| TYPE: DNA
| ORGANISM: B.fragilis
| US-09-540-209B-1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
Sequence 1521, Application US/09540209B
GENERAL INFORMATION:
APPLICANT: GATY L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT ETLING DATE: 2000-04-04
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US-09-528-682-1 x US-09-602-777A-227
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-528-682-1 x US-09-540-209B-1521
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 GCGGTGGCTCGGCGCGCACCCTCAACATGATCGATGCCACGGTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 uArg...LeuHisArgAsnArgGluTyrArgAspArgTyrTyrArgAsnL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 TACGCCTTTATCTGGGGCTGGGGATTTGCCGTGTTTGGTGTACTTCCACG 308
     109 rGluGlnGluValSerAlaLeuGlyGlyIleProTyrSerGlnIleTyrG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyValIleAspGl
                                                                                                            93
                                                                                                                                                                                                                                                                                                                    59 rValSerThrSerLeuSerLeuArgSerAlaHisLeuAlaGlyGlnSerI 76
                                                                                                                                                                                                                                                                                                                                                                                                                     50 ThrGlyPheValArgTyrAsp............AspGlyTy 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yCysGlyAsnSerSerArgThrIleThrGly 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspHisGlnAlaTrpArgGluGluProTrpIleHisHisAlaProGlnGl 186
                                                                                                                                                       leLeuSerGlyTyrSerThrTyrTyrIleTyrValIleAlaThrAlaPro 92
                                                                                                                                                                                                                                                                TTACCAGGCCGGGATTCCCTTGTCCCGCCAGAGGGGTGGCCAGCCCGTTTA 757
                                                                                                                                                                                                                                                                                                                                                                       ACGGGGTATGCCCGGTATGGTTGGGATTATAACCGTTTGTATGACTTGTA 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGCGGCTATCGACGACGCGTTTGCAGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTCT.....AGTGGTTGGCCTGCC 378
                                                                                                         AsnMetPheAsnValAsnAspValLeuGlyValTyrSerProHisProTy 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.50
0.891
40.092
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Gaps: 10
Percent Identity: 19.355
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                                                           ....AMAGTTATTGATCCGGATACCTG 812
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                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: GATY L. Breton

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELITIVE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1001-001

CURRENT APPLICATION NUMBER: US/09/540,209B

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 104444

SEQ ID NO 4973

LENGTH: 2847

TYPE: DNA
ORGANISM: B.fragilis
US-09-540-209B-4973
                                                                                                                                                                                                                alignment_block: us-09-540-209B-4973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-540-209B-4973
                                                                                                                                                                                                                                                                                         Quality:
Ratio:
Percent Similarity:
                                                                                                                                                            Align seg 1/1 to: US-09-540-209B-4973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1149 C 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1038 AACGATCGGGAAGCTGCGTGCGGCCGGTGTACCGTTCACGGTGGAAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1012 GAAAAA......GGAGGCTGC...CTGGGAGAGGA 1037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 gThrIle......ThrGlyAspThrC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 GluGluProTrpIleHisHisAlaProGlnGlyCysGlyAsnSerSerAr 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       954 CCGGGCGACAAGGGAGAACTACCTGGAGAAACTGAGGGTGAGC.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         813 GGGACGCATGGTCAGCCGGGTCAACGGCGTCAGTTTCGCCGGAATGTACG
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                                                           664 CGCAATAGCGGAGGATATATCCATACTTCTTCCGGCATCCGCTCCTGGCA 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....CAGAAATTCTGGAGA 1011
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                                                                                                         ArgTyrAspAspGlyTyrValSerThrSerLeuSerLeuArgSer....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ysAsnGluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGln 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 luAspGlyTyrArgLeuAlaGlyPheProProAspH1sGlnAlaTrpArg 175
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0.881
42.308
.....AlaHisLeuAlaGlyGlnSerIleL 77
                                                                                                                                                                                                                                                                                           Percent Identity:
                                                                                                                                                            from: 1
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11
23.077
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RELATING TO BACTEROIDES

8

1087

996

953

28

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alignment_scores:
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                                                                                                                                                                                      FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 41882
LENGTH: 1311
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 41882, Application US/60360039 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cao, Yongwei
                                                                                                                                                 ORGANISM: Thermoplasma acidophilum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTCCGGGCCTT.....GAAGAGCAGGCATGGACCATTGGAGAGTGG.. 1131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gLeuHisArgAsnArgGluTyrArgAspArgTyrTyrArgAsnLeuAsnI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTTACCATTTCGAGCCGGTTCGCCGCAAAGTCGGGATGGTTTATGATGT 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTGGACAGCCCTTGACAATGGTATTGCCTATGTCCGCAATAATTCGCTG 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTGGAGAATAATACCGTTCTGGGCCTGTATTGTGATATGGACAATAATA 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tPheAsnValAsnAspValLeuGlyValTyrSerProHisProTyrGluG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTTTCAGCAAAGAGGGACACTTGCTTTGGAAGGAGAATGCTGATAACCA 863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspThrCysAsnGluGluThrGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...AlaGlyPheProProAspHisGlnAlaTrpArgGluGluProTrpIl 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IleTyrGlyTrp.....TyrArgValAsnPheGlyValIleAspGluAr 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lnGluValSerAlaLeuGlyGlyIleProTyr.....SerGln 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....ThrAlaProAsnMe 94
                                                                                                                                                                                    DNA
     Quality:
Ratio:
     77.00
0.681
Length:
Gaps:
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     260
12
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US-09-528-682-1 x US-60-360-039-41882
                        seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-096-080-27
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                                                                             1105
                                                                                                                                                                                                                                                                                    1011 AAGGCCGGCCCTGTACGGCGCCAGGCACACGATAATCCCGGTCGGAGAGA 1060
                                                                                                                                                                                                                               172 lnAlaTrpArgGluGluProTrpIleHisHisAlaProGlnGlyCysGly 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              526 TTCAGGATCAACCCGGGTTTTGGCATGGGCGAATTCGCAGGTACCACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         388 CCGCCGGAGGACATACTCTACTCC......CCGAACAATGCCTC
                                                                                                                                                                                                                                                                                                                                                                                          961 GATGTGCACAACGGCTTCGCGGGCACAGACATCGGCATGAACCTCAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              911 CGGGACGCTATCTGGTTGGCGATGCCGGCATCATCGTCGGCACAGTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 TyrGlyTrpTyrArgValAsnPheGlyValIleAspGluArgLeuHisAr 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 yrGlu...GlnGluValSerAlaLeuGlyGlyIleProTyrSerGlnIle 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        626 CCTACAGAAAGGCCAGGGAGGACGGGATCAGGGAGTTCGGTATACACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576 CGGGGGTGCCAGGACAAAGTTCGGGATAGACCCGGATGCCGCCATCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 ACACTTTCACACAGTACAGGAAGATGAGGGAAAAGCCCGAGAGGATATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        426 CGAGTACGATCTCAACTTCGCGCTTGATCGCGGGATAGCCATAAACTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 oAsnMetPheAsnValAsnAspValLeuGlyValTyrSerProHisProT 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 ProProAspGluIleLysArgSerGlyGlyLeuMetProArgGlyHisAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACACGGACAGG.....ATCGGCGATACG 1128
                                                                                                                           AsnSerSerArgThrIleThrGlyAspThr
                                                                                                                                                                                 GGGTTGAGGGCGAGAAG.....ATCACCGTCACCGGGCAGATATGCGAG
                                                                                                                                                                                                                                                                                                                                     eAlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProProAspHisG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                .....ArgAsnLeuAsnIl 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ...GGCGAAAACGAACTGGACATTGCGGCACTGGGGGTCAGCCGTG....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IleLeuSerGlyTyrSerThrTyrTyrIleTyrValIleAlaThrAlaPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .TTGAAAGAATTT...GATCGATACCATTTCGGCGATCTCGTCCTCGAAC
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775

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150 910

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; NAME/KEY: CDS
; LOCATION: (101)..(865)
US-10-096-080-27
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; Sequence 27, Application US/10096080
; GENERAL INFORMATION:
seq_documentation_block:
                                             seq_name: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-42529
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Ratio:
Percent Similarity:
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SEQ ID NO 27
LENGTH: 1322
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TITLE OF INVENTION: Inhibitors of Formation of Protease Resistant Prion
TITLE OF INVENTION: Protein
FILE REFERENCE: 50121
CURRENT APPLICATION NUMBER: US/10/096,080
CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US/09/823,494
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/128,450
PRIOR APPLICATION NUMBER: 09/128,450
PRIOR APPLICATION SUMBER: 1998-08-03
NUMBER OF SEQ ID NOS: 29
NUMBER OF SEQ ID NOS: 29
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APPLICANT: Caughey, Byron W
APPLICANT: Chabry, Joelle
APPLICANT: Priola, Susette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hrIleThrGlyAspThrCysAsnGluGluThrGlnAsnLeuSerThrIle 209
                                                                                                                                                                                                                                                                                                                                                                                      CGTGCAC.....GACTGCGTCAATATCACCATCAAGCAGCACA 659
                                                                                                                                         rGlnSerGluValAspIleTyr 233
                                                                                                                                                                                            GATGTGAAGATGATGGAGCGCGTGGTGGAGCAGATGTGCGTCACCCAGTA 750
                                                                                                                                                                                                                                       TyrLeuArgGluTyrGlnSerLysValLysArgGlnIlePheSerAspTy 226
                                                                                                                                                                                                                                                                                     CGGTCACCACCACCAAGGGGGGAG.....AACTTCACCGAGACC 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGGAGCGCCGTGAGCAGGCCCATGATCCATTTTGGCAACGACTGGGAGG 536
                                                                                           CCAGAAGGAGTCCCAGGCCTAT 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGG......CCAGTGGATCAGTACAGCAACCAGAACAACTT 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgLeuAlaGlyPheProProAspHisGlnAlaTrpArgGluGluProTr 179
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1.149
54.032
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Sequence 42529, Application US/60360039

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT APPLICATION SEQ OZ-02-21
NUMBER OF SEQ ID NO 42529
LENGTH: 1437
TYPE: DNA
ORGANISM: Anabaena PCC7120
US-60-360-039-42529
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US-09-528-682-1 x US-60-360-039-42529
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                                                                                                                   1010 CTTGTCGTGAATATGCTAATCCCGACCGCTCAATGCTGGAATTAGTTCTA 1059
156 AlaProAlaGluAsp 160
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|060 GCTCCTGCCAAAGAT 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                            860 AGCAAATGGAGTTTTTCCAGAAGCTAGAAGGTTTAGAAGGCGTGCCAGTA 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            757
                                                                                                                                                                                                                              960 GTTGTTTTCGCGATCGCCCCTCCTCAGCGTTTATGCTGATATGAGCAACA 1009
                                                                                                                                                                                                                                                                                   910 ATTAACCTCCATCTGTGGTTTGATCGGAAATTAACAGACATTGATCACCT 959
                                                                                                                                                                                                                                                                                                                                                                                                    122 SerGlnIleTyrGlyTrpTyrArgValAsnPheGlyValIleAspGluAr 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          832 .....TTGAAAGTCATGTTGCCACAGCCTTGGC 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         676 GAACGGGGTGGAGAAGTCAGGCTCAACGCCCCTCTAAAAGAGATTTTGCT 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        790 ATTACG.....GCAGACTTTTACGTGTCAGCTATGGCAGTTGACCCC.. 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 nMetPheAsnValAsnAspValLeuGlyValTyrSerProHisProTyrG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 LeuSerGlyTyrSerThrTyrTyrIleTyrValIleAlaThrAlaProAs 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 pHisAlaArgGlyThrGlnThrGlyPheValArgTyrAspAspGlyTyrV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 AspArgGlyThrGlnMetAsnIleAsn.....LeuTyrAs
                                                                                                                                              .....ArgGluTyrArg......AspArgTyrTyrArgAsnLeuAsnIle 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....CTGCGCGGGTTAAATGGAGAGCCAGATGAAGTG 789
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1.041
47.742
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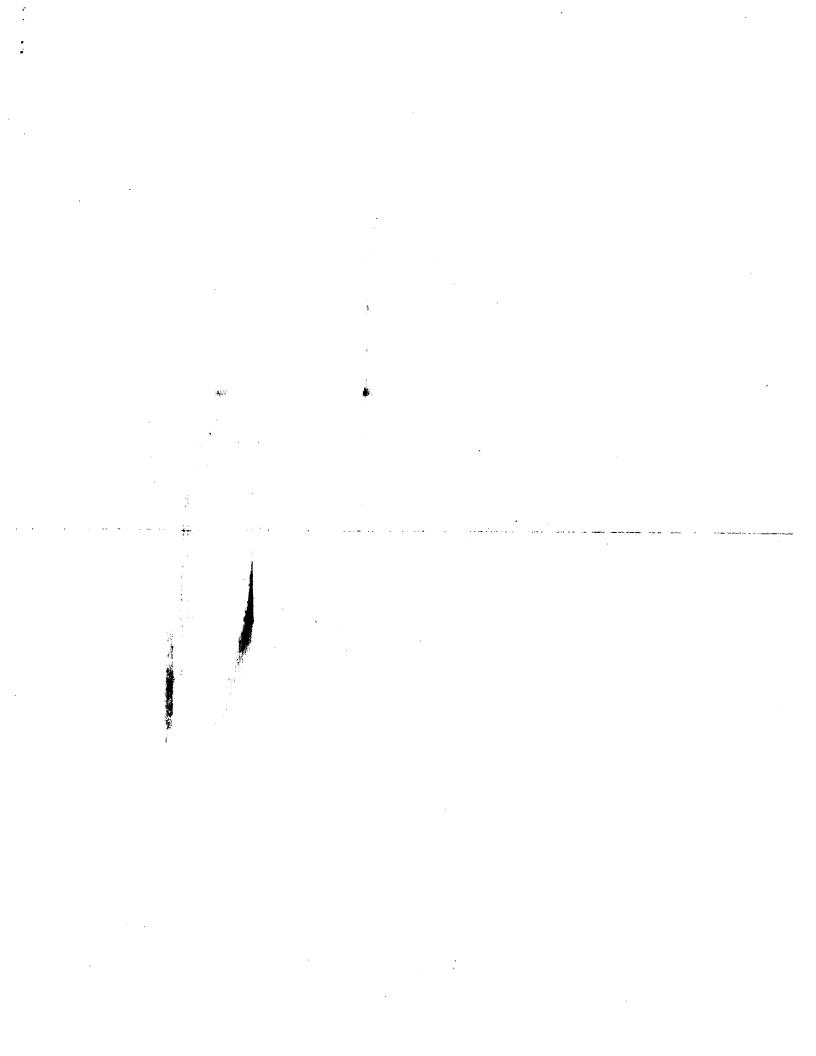
seq_documentation_block:

/cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-26535

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alignment_block:
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US-60-360-039-26535
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SEQ ID NO 26535
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APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
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                                                                                                        1954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1808 TAGAAGAAATTCGGCAACTGTTG...........CATAAAGGGGAA 1842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1674 CATTGATTATTTG......TGGAACCGTAACGCCATTGTGC 1708
                                                                                                                                                            159
                                                                                                                                                                                                                                                             142
                                                 175 gGluGluProTrpIleHisHisAlaProGlnGlyCysGlyAsnSerSerA 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGCGCCTATAAAATTAGCTATTTCTACGATGCGGCGATCGCCCCTAACC 1807
     G......GGTAACACCCTTT 2017
                                                                                                        GAGCACGTTTTCACCGCCGGAGGATCGGGAGCCGACGAAGATATGATGCG 2003
                                                                                                                                                       GluAspGlyTyrArgLeuAlaGlyPheProProAspHisGlnAlaTrpAr 175
                                                                                                                                                                                                        CCAAAGGCTATGCTGTGCGTTGGTTGAGCCAACAGTGGAATATTCCCCTG 1953
                                                                                                                                                                                                                                                       snArgGluTyrArgAspArgTyrTyrArgAsnLeuAsnIleAlaProAla 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uSerGlyTyrSerThrTyrTyrIleTyrValIleAlaThrAlaProAsnM 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isAlaArgGlyThrGlnThrGlyPheValArgTyrAspAspGlyTyrVal 60
                                                                                                                                                                                                                                                                                                                                                        pTyrArgValAsnPheGlyValIleAspGluArgLeu.....HisArgA 142
                                                                                                                                                                                                                                                                                                                                                                                                       CAAACCGTAAATACCATC......1860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ......CTCCAACCCAAGGAAGAACT 1757
                                                                                                                                                                                                                                                                                                            .....ATTTCCTTTGGTCAATTTTTGGATATTCTGCCCATCCGAGCTT 1903
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141 ArgAsnArgGluTyrArgAspArgTyrTyrArgAsnLeuAsnIleAlaPr 157
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Sequence 1307. Application US/10104047
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-10-104-047-1307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1307
LENGTH: 2405
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1564
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1734 TGGCCTCCTGGTATGAGCAG.....GGGATCCTT...GAGAACATCCAG
                                                                                                   1714 CCAGTACATGGAG...
                                                                                                                                                                                                 1679
                                                                                                                                                                                                                                                                                                                                                                                                1591 GGTGGCCATCAGCTCCAAATTTGAGACCCGGGAG.......GATA 1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1515 TCACCATGGCAACCTTCACCATGACGCTGGCACGGGTCTGCCTCTGCCC. 1563
                                             124 leTyrGlyTrpTyrArgValAsnPheGlyValIleAspGluArgLeuHis 140
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                                                                                                                                                                                                                                            91 AlaProAsnMetPheAsnValAsnAspValLeuGlyValTyrSerProHi 107
                                                                                                                                                                                                                                                                                                                                             74 lnSerIleLeuSerGlyTyrSerThrTyrTyrIleTyrVallleAlaThr 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AspSerArgProProAspGluIleLysArgSerGlyGlyLeuMetProAr
                                                                                                                                              sProTyrGluGlnGluValSerAlaLeuGlyGlyIleProTyrSerGlnI 124
                                                                                                                                                                                            GTCCCT.....GATGGCATCGTGGCCTTCTACACCAGCTA 1713
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51.337
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Gaps: 11
Percent Identity: 23.529
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seq_documentation_block:
Sequence 39204, Application US/60360039
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 2559
TYPE: NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
Quality:
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; ORGANISM: Xanthomonas campestris
US-60-360-039-39204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-528-682-1 x US-60-360-039-39204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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                                                                      1091
                                                                                                                                          1898 GTGTCCGA 1905
1141 GGCATCACCTACCAGAAGGGTGCGGCGGTGCT 1172
                                                                                                                                                                                                                                                       156
                                                                                                        168
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                                                                                                                                                                                                                                                                                       129 ArgValAsnPheGlyValIleAspGluArgLeuHisArgAsn...... 142
                                                                                                                                                                                                                 991 AAGATCACCATGCAGCTGCACCCGGAATACCGTGCCAATCTGGACCGCAT 1040
                                                                                                                                                                                                                                                                                                                                                           891 CGCGCACGAGCTGGCGCACCAGTGGACCGGCGACACCGTCACCATGGCGT 940
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                                                                    ..HisHisAlaProGlnGlyCysGlyAsnSer 190
                                                                                                                                                                         .....ProAlaGluAspGlyTyrArgLeuAlaGlyPhe..... 167
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Gaps:
Percent Identity:
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4
27.660
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9b_ba:VCTTVANB21
9b_ba:VIRCTYANB8
9b_ba:VCTTVANB5
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9b_ba:FA115708
9b_ba:AFA114369
9b_bh:AFA1424
9b_ba:ECOELTA2
9b_ba:ECOELTA2
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gb_pat:AR118598
gb_ba:VIBCTXA
gb_pat:E00132
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9b_ba:ECITA
9b_pat:A06082
9b_pat:A06083
9b_pat:A02701
9b_pat:A02702
9b_ba:AF452584
9b_ba:AF463401
9b_ba:VIBCTXABA
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gb_pat:E00613
gb_pat:A16419
gb_pat:AR118597
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9b_pat: A04913

9b_ba: ENSLTPA

9b_ba: ENRLTPA

9b_pat: E03421

9b_pat: E03421

9b_ba: A8011677

9b_ba: ECOTOXA

9b_ba: S60731

9b_pat: A04915
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Database length: 1873333701
Search time (sec): 1859.660000
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Query: US-09-528-682-1
Query length: 240
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-FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX-oligo
-TRANS=human40.cdi -LIST=1000 -DOCALIGN=200 -THR_SCORE-quality
-THR_MIN=1 -ALIGN=50 -MODE-LOCAL -OUTPMT=PST -NORM-ext
-HEAPSIZE=500 -MILEN=0 -MATRIX-oligo
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-USER=US09528682_@CGN1_1_6642 -NCPU=6 -ICPU=3 -LONGLOG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XGAPOP and YGAPOP must be equal. Assuming YGAPOP-XGAPOP-60.000 XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT-XGAPEXT-60.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenEmbl:*
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.0e-190
.0e-190
.0e-185
.6e-111
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.0e-83
.5e-27
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          866
898
1148
1434
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777
RED3421 DNA encoding LTh of ent AB011677 Escherichia coli gene K01995 E. coli toxA gene encodin S60731 heat Labile enterotoxin A04915 Artificial sequence LTA M7244 plasmid EWD 299 (from E. E00613 DNA encoding A component A16419 A subunit of a labile tox AR118597 Sequence 5 from patent V00275 E. coli LT87 gene for hea A06083 pEBK620 HindII-fragment A06083 pEBK620 pHindII-fragment A06083 pHindII-fragment A06083 pHindII-fragment A06083 pHindII-fragment A06
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1 AF242417 Escherichia coli heat.

1 M35581 Plasmid P307 (from E.coli M35581 Plasmid ENT P307 (enterol M15361 Plasmid ENT P307 (enterol M15361 Plasmid ENT P C086 (enterol M15361 P C086 P
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gb_p1:BLYACPIII
gb_p1:RS28259
gb_sts:G52559
gb_sts:G52559
gb_pr:HSS337370
em_htgo_inv:ACO32116
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em_htgo_inv:ACO4680
gb_pat:AX251599
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em_htgo_inv:ACO657411
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em_htgo_inv:ACO657682
gb_p1:AK026527682
gb_p1:AK026537
gb_p1:AK0263637
gb_p3:EM037663
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9b_ro:AC087184

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9b_pat:A16408
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gb_pat: AR118626
gb_pat: I42977
gb_pat: DAZ84452
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9b_htg:AC073176
9b_htg:AC073176
9b_htg:AC106284
9b_htg:AC106284
9b_htg:AC073368
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gb_ba:AE009014
gb_ba:AE007980
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gb_ba:ECOETOXHL
gb_pat:AR019034
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gb_ba:VCCTXAB2
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I J01847 Vibrio cholerae chole
I K01170 Vibrio cholerae toxA
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I M17873 E.coli (from pig) hea
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| 142977 Sequence 5 from patent
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| Ac029067 Glardia intestinali
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| AF7882582 Homo sapiens clone
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Submitted (07-MAR-2000) Botany,
Roosevelt Road, Sec. 4, Taipei,
Location/Qualifiers
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Chang, G.N. and Ho, K.C.
Heat-labile enterotoxin subunit A
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Escherichia coli heat-labile
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(from E.coli) heat-labile te cds.

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DNA

BCT 24-APR-1996

enterotoxin linear

(clone: 1ta gene.

pAT153.)

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/transl_table=11
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E.coli LTA gene for labile toxin
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Patent: EP 0145486-A 5 19-JUN-1985;
GLAXO GROUP LIMITED
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Escherichia coli
Bacteria; Proteobacteria; gamma
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REYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPGGCGNSSRTITGDTCN
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MI5362.1 GI:148337
LTP gene; heat-labile toxin.
Plasmid ENT (enterotoxigenic
p370.
                                      Plasmid ENT P307 (enterotoxigenic M15362
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yGlyTleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyV 134
                                 TTAGGCGTATACAGCCCTCACCCATATGAACAGGAGGTTTCTGCGTTAGG
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Escherichia coli and Vibrio cholerae
J. Bacteriol. 169, 1352-1357 (1987)
87137303
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REYRDRYYRNLNIAPAEDGYRLAGFPDHQAWREEPWIHHAPQGCGNSSRTITGDTCN 
EETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL"
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/db_xref="taxon:2463"
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                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto, T., Gojobori, T. and Yokota, T. Evolutionary origin of pathogenic determinants Escherichia coli and Vibrio cholerae Ol Bacteriol. 169, 1352-1357 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCG86.
Plasmid ENTR
Unreported.
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                  289
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REYRDRYYRNLNIAPAEDGYRLAGFPDHQAMREEPWIHHAPOGCGNSSRTITGDTCN
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122. .175
                                                                                                                                                                                                                               /note="Heat labile toxin 122. .898
                                                                                                                                                                                                              /note="Heat labile toxin
                                                                                                                                                                                                                                                                                                              /organism="Plasmid ENTR"
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               /product="Heat labile toxin subunit A"
155 c 186 g 268 t
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           snArgIleArgAspGluLeu
                                                         sValLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA
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ACAGAATTCGGGATGAATTA
                                            AGTTAAGAGGCAGATATTTTCAGACTATCAGTCAGAGGTTGACATATATA
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seq_name:

gb_pat:E03421

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KITASATO INST:THE
OS Escherichia coli
PN JP 1992079898-A/1
PD 13-MAR-1992
PF 23-JUL-1990 JP 1990194208
PI DANBARA HIROFUMI, ABE AKIO
PC C12Q1/68,C07H21/02,C07H21/04,C12N15/11,C12N15/31,C12Q1/04
C12Q1/10,
PC (C12N15/31,C12R1:19),(C12Q1/04,C12R1:63,C12R1:19); CC
Strandedness: Double;
CC topology: Linear;
CC topology: Linear
TTATACCGTGCTGACTCTAGACCCCCAGATGAAATAAAACGTTCCGGAGG
                                                                                                                      LeuTyrArgAlaAspSerArgProProAspGluIleLysArgSerGlyGl
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Danbata, H. and Abe, A.

DNA AND RNA PROBE TO SIMULTANEOUSLY DETECT VIBRIO CHOLERATE AND ENTEROTOXIGENIC ESCHERICHIA COLI AND DETECTION OF VIBRIO CHOLERA AND ENTEROGEXIGENIC ESCHERICHIA COLI USING THE SAME DNA AND RNA
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DANBARA HIROFUMI, ABE AKIO

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774. .1148
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138 rgLeuHisArgAsnArgGluTyrArgAspArgTyrTyrArgAsnLeuAsn 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProProAspHi 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCTCAGATATATGGATGGTATCGTGTTAATTTTGGTGATGATGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leAlaThràlaProAsnMetPheAsnValAsnAspValLeuGlyValTyr 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_ba:AB011677
                                                                                                                                Submitted (02-MAR-1998) Katsuhiro Komase, The Kitasato Institute, Center for Basic Research, Lab. of Virology; Shirokane 5-9-1, Centor for Basic Research, Lab. (F-mail:komase-k@kitasato.or.jp, Minato-ku, Tokyo 108-8642, Japan (F-mail:komase-k@kitasato.or.jp, Tel:+81-3-3444-6161, Fax:+81-3-3444-6637)
                  Tamura,S., Asanuma,H., Tomita,T., Komase,K., Kawahara,K., Danbara,H., Hattori,N., Watanabe,K., Suzuki,Y., Magamine,T., Aizawa,C., Oya,A. and Kurata,T.
Escherichia coli heat-labile enterotoxin B subunits supplemented
                                                                                                                                                                                                                                                                                                                                                             AB011677.1 GI:3062900 heat-labile enterotoxin A subunit; LTh a subunit; enterotoxin A subunit; LTh a subunit. Escherichia coli (strain:1032 (Enterotoxigenic)) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      subunit, complete cds
AB011677
                                                                                                                                                                                                                                                                                                                                     Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli genes
with a trace amount of the holotoxin as an
                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                              Escherichia
                                                                                                                                                                                                                                               Komase, K.
                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                           (sites)
                                                                                                                                                                                                                                                                      (bases 1 to 1434)
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adjuvant
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                                                                                                                                                                                                                                                                                                                     Enterobacteriaceae;
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A subunit and B
for nasal
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alignment_block:
US-09-528-682-1 x AB011677
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Ratio: 1.000
Percent Similarity: 100.000
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MEDLINE
                                                         407
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SerProH1sProTyrGluGlnGluValSerAlaLeuGlyGlyIleProTy
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                                                                                                                                                  \AlaGlyGlnSerIleLeuSerGlyTyrSerThrTyrTyrIleTyrValI
                                                                                                                                                                                                                                                                                                                                                TCTTATGCCCAGAGGGCATAATGAGTACTTCGATAGAGGAACTCAAATGA
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                                                       TAGCGACAGCAAATATGTTTAATGTTAATGATGTATTAGGCGTATAC
                                                                                                                                                                                                                                      TyrAspAspGlyTyrValSerThrSerLeuSerLeuArgSerAlaHisLe
                                                                                                                               Vaccine 12 (12), 1083-1089 (1994) 95091056
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864. .1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="1032 (Enterotoxigenic)"
/db_xref="taxon:562"
91. .867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MNKVKCYVLFTALLSSLCAYGAPQSITELCSEYRNTQIYTINDK
ILSYTESMAGKREMVIITEKSGATFQVEVPGSQHIDSQKKAIERMKDTLRITYLTETK
IDKLCYWNIKTPNSIAAISMEN"
258 c 286 g 402 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="heat-labile enterotoxin
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/db_xref="GI:3062902"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRN
REYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCGNSSRTITDDTCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mknITF1FF1LLASPLYANGDKLYRADSRPPDE1KRSGGLMPRG
HNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSLSLRSAHLAGQS1LSGYSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="heat-labile enterotoxin A subunit"
/protein_id="BAA25725.1"
/db_xref="GI:3062901"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EETQNLSTIYLRKYQSKVKRQIFSDYQSEVDIYNRIRDEL"
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Gaps:
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BASE COUNT
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                                        alignment_scores:
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rgLeuH1sArgAsnArgGluTyrArgAspArgTyrTyrArgAsnLeuAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAAGCTTGGAGAGAACCCCTGGATTCATCATGCACCACAAGGTTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATTACATCGTAACAGGGAATATAGAGACCGGTATTACAGAAATCTGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enterotoxin; heat-labile enterotoxin; toxA gene.
E.coli H10407 (serotype 078:H11) plasmid DNA, clone
Escherichia coli
                     Quality:
                                                                                                 298 a 10
46 bp upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamamoto,T., Tamura,T. and Yokota,T. Primary structure of heat-labile enterotoxin Escherichia coli pathogenic for humans J. Biol. Chem. 259, 5037-5044 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This heat-labile enterotoxin is pathogenic for humar Compared in [1] with LTP A and CT A (LTP-pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CT-cholera toxin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia.
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                                                                                                                                                                                                    /note=
184.00
                                                                                                 /product="heat-labile enterotoxin A2"
165 c 186 g 285 t
tream of FokI recognition pattern.
                                                                                                                                                              /product="heat-labile enterotoxin Al" 794. .931
                                                                                                                                                                                                                                              158.
                                                                                                                                                                                                                                                                                /PIOCEIN_Id="AAA24685.1"
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/DIOCEIN_Id="AAA24685.1"
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IYVLATAPNHENVNDVLGVYSHHPYEDEVSALGGIPYSGIYGWYRVNFGVIDERLHRN
REYKDRYYRNLNIAPAEDGYKLAGFPPDHQAMREEPMIHHAPQGCGDSSRTITGDTCN
                                                                                                                                                                                                                                                               EETQNLSTIYLRKYQSKVKRQIFSDYQSEVDIYNRIRNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Escherichia coli"
/db_xref="taxon:562"
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                       Length:
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Similarity:

100.000

Percent

Identity:

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SOURCE
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VERSION
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US-09-528-682-1 x ECOTOXA
                                                                                                                                                                                         seq_documentation_block:
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                                                                                                                                                                                                                         seq_name: gb_ba:S60731
                                                                                                                                 KEYWORDS
                                                                                                                                                                              DEFINITION
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 JOURNAL
MEDLINE
                                               AUTHORS
TITLE
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Inoue, T., Tsuji, T., Koto, M., Imamura, S. and Miyama, A. Amino acid sequence of heat-labile enterotoxin from centerotoxigenic Escherichia coli is identical to that strain H 10407 FEMS Microbiol. Lett. 108 (2), 157-161 (1993) 93252225
                                                                                                                                                                 S60731 1275 bp DNA linear BCT 29 heat-labile enterotoxin A subunit, heat-labile enterotoxin subunit [Escherichia coli, 21d, Genomic, 1275 nt].
                                                                                            Escherichia coli
Bacteria; Proteobacteria;
                                                                                                                   Escherichia coli 21d
                                                                                                                                           S60731.1 GI:408994
                                                                                                                                                      subunit [Escherichia s60731
                                                                                  Escherichia.
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                                                                            TyrAspAspGlyTyrValSerThrSerLeuSerLeuArgSerAlaHisLe 71
                                    SerProHisProTyrGluGlnGluValSerAlaLeuGlyGlyIleProTy 121
                                                                                                                                                                         TATGATGACGGATATGTTTCCACTTCTCTTAGTTTGAGAAGTGCTCACTT
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REYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCGDSSRTITGDTCN
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seg_documentation_block:
LOCUS
DEFINITION Artificial sec
ACCESSION A04915
VERSION A04915.1 GI:
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthetic construct.

M synthetic construct
artificial sequence.
1 (bases 1 to 777)
Hayes, M.V., Harford, S. and Ross, G.W.
Microbiological process
Patent: EP 0145486-A 7 19-JUN-1985;
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Ratio:
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135 c 164 g 222 t 1 others
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AUTHORS
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M57244 J05702

M57244 I GI:531190

enterotoxin; heat-labile e

plasmid EWD 299 DNA.

Plasmid EWD 299
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On Aug 20
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                                                                                                                                                                                                                                 20, 1994 this sequence Location/Qualifiers
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KEYWORDS
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                                                                                                            TITLE
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 GLAXO GROUP LITD
OS ESCHETÍCHIA
PN JP 19860050
PD 10-JAN-1986
PF 12-DEC-1984
PR 12-DEC-1984
PR 12-DEC-1984
PR 12-DEC-1984
                                                                                                                                                                                                                E00613.1 GI:2168892
JP 1986005097-A/1.
Escherichia coli.
                                                                                                          MICROBIAL METHOD
Patent: JP 1986005097-A
                                                                                                                                                                        Bacteria; Proteobacteria; Escherichia.
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Maikuru, B.H., Suteiibun, H.
                                                                                                                                                                                                   Escherichia coli
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            Escherichia coli
JP 1986005097-A/1
10-JAN-1986
12-DEC-1984 JP 1984262645
12-DEC-1983 GB 83 8333131
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MAIKURU BIKUTAA HEIZU, SUTEIIBUN HAAFUOODO,
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/note="a"
/citation=[1]
/replace=""
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GYRLAGFPPDHQAWREEPWIHHAPQGCGNSSRTITGDTCNEETQNLSTIYLREYQSKV
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SOURCE
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Quality: 97.00
Ratio: 1.000
Percent Similarity: 100.000
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LOCUS A16419
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Escherichia coli
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                       Bacteria; Proteobacteria;
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hypothetical: No;
anti-sense: No;
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C07K15/04, A61K39/108, C12N1/20, C12N15/00//C12P21/00, (C12N1/20
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(C12R15/00,C12R1:19);
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Location/Qualifiers
1. .777
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/db_xref="taxon:562"
137 c 163 g 222 t
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Gaps: 0
Percent Identity: 100.000
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                        gamma subdivision; Enterobacteriaceae;
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ORIGIN
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LOCUS AR118597
                                                                                                                                                                                                             seq_name: gb_pat:AR118597
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                  Sequence 5 from patent US ARI18597
1 (bases 1 to 711)
Domenighini,M., Rappuoli,R., Pizza,M. and
Immunogenic detoxified mutants of cholera
                                                                   Unknown
                                                  Unclassified
                                                                                    Unknown
                                                                                                                  AR118597.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Escherichia
/db_xref="taxon:562"
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/db_xref="GI:641009"
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   of the toxin
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AUTHORS
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SOURCE
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seq_documentation_block:
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Percent Similarity: 100.000
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V00275 J01604
V00275.1 GI:41339
enterotoxin; signal peptide.
Escherichia coli.
                                                                                                                                                                                                                                                                                               Escherichia coli
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                    J. Biol. Chem. 257 (10),
                                                                                                                                                                                                                                     Spicer, E.K. and Noble, J.A. Escherichia coli heat-labile enterotoxin.
                                                                                                                                                                                                                                                                                        Escherichia.
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                                                  /product="messenger 90. .143 90. .854
                                                                                                /organism="Escherichia
/db_xref="taxon:562"
56. .>868
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123 c 156 g
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                   595 bp DNA li
E.coli LT87 gene for heat-labile enterotoxin.
X83966
                                               Submitted (17-JAN-1995) Y. Germani, Institut Pasteur, Roux, F-75724 Paris Cedex 15, FRANCE Related sequence: M15361-3 (Yakamoto).

Location/Qualifiers
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Escherichia coli
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dryyrnliniapaedgyrlaegeppdhqmreeppihhapqgcgdssrtitgdtcneetq 

nlstiylreygskykrqifsdygseydiynrirdel" 

142 c 179 g 263 t
/organism="Escherichia coli"
/strain="ETEC LT 87"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetic construct.
synthetic construct
artificial sequence.
artificial sequence.
1 (bases 1 to 791)
Ceska,M., Kricek,F., Hoegenauer,G. and Besemer,J.
Plasmids and bacteria strains, and method of preparing
Patent: EP 008452-A 1 27-JUL-1983;
SANDOZ AG; SANDOZ-PATENT-CMBH; SANDOZ-ERFINDUNGEN
Verwaltungsgesellschaft m.b.H
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205. .579
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1 (bases 1 to 791)

Ceska, M. Kricek, F., Hoegenauer, G. and Besemer, J.

Plasmids and bacteria strains, and method of preparing

Patent: EP 0084522-A 2 27-JUL-1983;

SANDOZ AG, SANDOZ-PATENT-GMBH, SANDOZ-ERFINDUNGEN

Verwaltungsgesellschaft m.b.H
                                                                                                                                                                                    Synthetic DNA sequence A02701
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synthetic construct
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                                                                 Patent:
                                                              NEW PLASMIDS AND BACTERIAL STRAINS AND PRODUCTION PROCESS THEREO PATENT: WO 8302456-A 1 21-JUL-1983;
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/organism="synthetic construct"
/db_xref="taxon:32630"
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                                      Location/Qualifiers
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                           seq_documentation_block:
LOCUS AF452584
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US-09-528-682-1 x A02702/rev
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Ratio: 1.000
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synthetic construct
artificial sequence.
1 (bases 1 to 795)
Vibrio cholerae
AF452584
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A02702.1 GI:344646
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/db_xref="taxon:32630"
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Unpublished
2 (bases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (29-NOV-2001) Department of Epidemiology and Preventive Medicine, University of Maryland School of Medicine, and VA Maryland Health Care System, Warehouse at Camden Yards, 322 W. Camden Street, Suite 675, Baltimore, MD 21201, USA
                                                                                Vibrio cholerae strain 571-88
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                                       AF463400.1 GI:18448888
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1 (bases 1 to 777)
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RGYRDRYYSNLDIAPAADGYGLAGFPPEHRAMREEPWIHHAPPGCGNAPRSSMSNTCD
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/db_xref="taxon:666"
/db_xref="taxon:666"
/note="identical sequence found in Vibrio cholerae strains
571-88 (serogroup O105) and 203-93 (serogroup O141)
serogroup: O37"
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129 c 169 g 236 t
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Li,M., Chen,Y., Kotetishvili,M., Stine,O.C., Morrow, Sulakvelidze,A. and Sozhamannan,S.
Genetic Analysis of the Virulence Regions, CTX f prophage and Vibrio Pathogenicity Island (VPI), in Diverse, Non-epidemic Serogroup Strains of Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae
                                     Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio. 1 (bases 1 to 777)
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Sulakvelidze, A. and
                     Li,M.,
                                                                                                  Vibrio cholerae
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RGYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIHHAPPGCGNAPRSSMSNTCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDTHNRIKDEL"
129 c 169 g 236 t
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/db_xref="taxon:666"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="ctxA"
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Percent Identity:
  Sozhamannan, S.
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3 CtxA
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                     Stine, O.C.,
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100.000
                                                                                                                                                                                  gene,
                                                                                                                                                                                                     linear
                       Morris, J.G. Jr.,
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                                                                                                                                                                                    complete
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JOURNAL REFERENCE
                                                                                                                                                                                                                                                                                                               Seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-528-682-1 x AF463401
                                                                                                         REFERENCE
                                                                                                                                                                                    SOURCE
                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_ba:VIBCTXABA
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                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                          DEFINITION
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Ratio: 1.000
Percent Similarity: 100.000
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                                           TITLE
                                                                                                                                              ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
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                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 AATGAGTACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCA 185
                                                                                                                                                                                                                                                                                                                                                                                                              44 SAlaArgGlyThrGlnThrGlyPheValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 ASnGluTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHi 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-DEC-2001) Department of Epidemiology and Preventive Medicine, University of Maryland School of Medicine, and VA Maryland Health Care System, The Marebouse at Canden Yards, 322 W. Camden Street, Suite 675, Baltimore, MD 21201, USA
Comparison of cholera toxin genes (ctxAB) of non-O1 vibrio cholerae strains 854 (O139-bengal) and S7 (O37) from two outbreaks Unpublished (1994)
                                                                                                                                                           ADP-ribosyltransferase; cholera toxin. Vibrio cholerae (sub_species 037, stra DNA, clone pKY310.
                                                                                                                                                                                                                                                 complete cds.
D30052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetic Analysis of the Virulence Regions, CTX f prophage and Vibrio Pathogenicity Island (VPI), in Diverse, Non-epidemic Serogroup Strains of Vibrio cholerae
                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
1 (bases 1 to 1372)
                                                                                                                                              Vibrio cholerae
                                                                                                                                                                                                                                D30052.1 GI:487332
                                                                                                                                                                                                                                                                                        Vibrio cholerae ctxA gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                              Honda, T
                                                                               Yamamoto, K., Do, V.G., Xu, M., Iida, T., Miwatani, T., Albert, M.J. and
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RGYRDRYKFLDEYGSKYKRQIFSGYQSDIDTHNRIKDEL"
a 129 c 169 g 236 t
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                  S7) (library: plasmid)
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alignment_block:
US-09-528-682-1 x VIBCTXABA
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                                                                                                                                       Align seg 1/1 to: VIBCTXABA
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                                                             248 AATGAGTACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCA
44 sAlaArgGlyThrGlnThrGlyPheValArg
                                                                                  AsnGluTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHi 44
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                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (29-Apr-1994) to DDBJ by:
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                                                                                                                                                                                                                                                          Ratio:
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06-879-8277
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="miklkfgyfftvllssayahgtpqnitdlcaeyhntqihtlndk
rlsyteslagnremalitfkngatfqyevpgsqhidsqkkaiermkdtlriaylteak
yeklcywnktphaiaaisman"
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RGYRDRYYSNLDIAPDADGYGLAGFPPEHRAMREEPMIHHAPPGCGNAPRSSMSNTCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="cxtA"
113. .889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="cholera toxin"
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/codon_start=1
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LOCUS AR118598
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LOCUS A16422
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                                                                                                                                                               ACCESSION
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      JOURNAL
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                                                                                                                                                                                                                                                                                135 AAGAGGAACTCAGACGGGATTTGTTAGG
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                                                                                                                                                                                                                                                                                                                                          TGCAAGAGGAACTCAGACGGGATTTGTTAGG
                                                                                                                                                                                                                                              gb_pat:AR118598
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1 (bases 1 to 723)

Domenighini,M., Rappuoli,R., Pizza,M. and Hol,W.

Immunogenic detoxified mutants of cholera toxin and of the toxin

LT, their preparation and their use for the preparation of vaccines

Patent: US 6149919-A 7 21-NOV-2000;
                                                                                                 Unknown
                                                                                                                                                               Sequence 7 from patent US AR118598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
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                                                                                                                   Unknown.
                                                                                    Unclassified
                                                                                                                                                  AR118598.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent:
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/protein_id="CAA01281.1"
/protein_id="CAA01281.1"
/db_xref="GG1:641011"
/translation="NDDKLYRADSRPPDEIKQSGLMPRGQSEYFDRGTQMNINLYDH
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ARGTQTGFVRHDDGYVSTSISLRSAHL/GQTTLKSGLSTYYYIYYLATAPMMENVNDVLG
ARSTPDEWSALGGIPYSQIYGMYRVHFGVLDEQLHRNRGYRDRYYSNLDIAPAAD
GYGLAGFPPEHAWREEPWIHHAPPGCGNAPRSSISNTCDEKTQSLGVKFLDEYQSKV
KRQIFSGYQSDIDTHNRIKDEL"
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/db_xref="taxon:666"
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US-09-528-682-1 x AR118598
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Quality: 26.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                             189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 777)
Lockman, H.A., Galen, J.E. and Kaper, J.B.
Vibrio cholerae enterotoxin genes: Nucleotide sequence analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP-ribosyltransferase; enterotoxin. V.cholerae (El Tor strain 62746) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is reported [1] to be identical to that for strains El Tor 2125 and .569B. the 'ttttgat' sequence repeated four times beginning at position 38 and once more at 101 is correlated with the amount of enterotoxin produced in various strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding ADP-ribosyltransferase J. Bacteriol. 159, 1086-1089 (1984)
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IYYIATAPNMFNVNDYLGAYSPHPDEQEYSALGGIPYSQIYGWYRVHFGYLDEQLHRN
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1. .723
                                                                                                                                                                                                                                       /transl_table=11
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                                                                                                                             /product="enterotoxin subunit A1"
119 c 164 g 257 t
                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                /note="enterotoxin prepeptide"
                                                                                                                                                                                                                                                                                                                                                                    /note="enterotoxin signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Vibrio cholerae"
/db_xref="taxon:666"
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125 c 163 g
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US-09-528-682-1 x VIBCTXA
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LOCUS E00132
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     139 GAGTACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCATGC 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent: JP 1183222033-A 1 23-DEC-1983;
SMITH KLINE RIT
OS cholera(Vibrio)
PN JP 198322033-A/1
PD 23-DEC-1983
PF 23-MAY-1983 JP 1983091416
PR 24-MAY-1982 US 82 381083
PI ARUFUOORU NIJIERU, DO BUIRUDO MISHIE
PC A61K39/106,A61K39/00,C07H21/04,C12NI
CC strandedness: Double;
CC topology: Linear;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FH CDS 1.777
FT CDS 1.777
FT CDS 1.777
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Arufucoru, N. and Do, B.M.
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ARUFUOORU NIJIERU, DO BUIRUDO MISHIERU
A61K39/106, A61K39/00, C07H21/04, C12N15/00;
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                                                                                                                                                                                                                                                                                                                       /product='subunit B
                                                                                                                                                                                                                                                                          /db_xref="taxon:32644"
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                                                                                                                                                                                                                                                              184 c
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-10_signal
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Vibrio cholerae
Bacteria; Proteobacte
1 (bases 1 to 1362)
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Direct Submission
Submitted (25-MAR-1991) E. Dams, Laboratory of Human Biochemistry,
Submitted (25-MAR-1991) Gruenenburgerlaan 171, B-2020 Antwerp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Correction of the cholera toxin nucleotide sequence of the Vibrio cholerae eltor strain 2125 \,
                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cholera toxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 1362)
Dams, E., De Wolf, M. and Dierick, W.
                  Ratio:
26.00
1.000
100.000
                                                                                                               /product="cholera toxin B
205 c 276 g 426
                                                                                                                                                                                                                                                                                                                                                                                                        IYVIATAPNMFNVNDVLGAYSPHPDEQEVSALGGIPYSQIYGWYRVHFGVLDEQLHRN
RGYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIHHAPPGCGNAPRSSMSNTCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_type=TANDEM
                                                                                                                                                              VEKLCVWNNKTPHAIAAISMAN"
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/translation="MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIYTLNDK
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/protein_id="CAA41593.1"
                                                                                                                                                                                                                                                                                                                                                                                           EKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDTHNRIKDEL"
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QSEYFDRGTQMNINLYDHARGTQTGFVRHDDGYVSTSISLRSAHLVGQTILSGHSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="pRIT10824"
72. .92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Vibrio cholerae"
/strain="eltor 2125"
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1. .1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:666"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteobacteria;
                                                                                                                                                                                                                            'db_xref="GI:48422"
                                                                                                                                                                                                                                                                                                                                          /product="cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="SWISS-PROT:P01555"
                                                                                                                                                                                                                                                                                            'codon_start=1
 Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma subdivision; Vibrionaceae; Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54
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                                                                                                                                                                                                                                                                                                                                          toxin A protein (CTA)"
                                                                                                                protein (CTB)"
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US-09-528-682-1 x VCTOXAB21
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LOCUS VIBCTXABB
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                                       sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                            source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aArgGlyThrGlnThrGlyPheValArg 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (29-APR-1994) Koichiro Yamamoto, Osaka University, Institute for Microbial Deseases, Department of Bacterial Infections; 3-1 Yamadaoka, Suita, Osaka 565, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Comparison of cholera toxin genes (ctxAB) of non-Ol vibrio cholerae strains 854 (O139-bengal) and S7 (O37) from two outbreaks Unpublished (1994)
2 (Dases 1 to 1369)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP-ribosyltransferase; cholera toxin.
Vibrio cholerae (sub_species 0139-Bengal, strain 1854) (library:
plasmid) DNA, clone pKY340.
Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D30053.1 GI:487333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Osaka University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koichiro Yamamoto
Institute for Microbial Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (29-Apr-1994) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Honda, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto, K., Do, V.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio. 1 (bases 1 to 1369)
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06-879-8277
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                                       110.
                                                                      /translation="MVKIIFWFFIFLSSFSY.ANDDKLYRADSRPDEIKQSGGLMPRG
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                                                                                                                                                                                                                                                                                                 110.
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883. .1257
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/db_xref="GI:808901"
                                                                                                                                                                                                                                                                                                                              /sub_species="0139-Bengal"
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                                                                                                                                                                                                                                            /gene="ctxA"
                                                                                                                                                                                                                                                                              /gene="
                                                                                                                                                                                                                                                                                                                 /clone_
                                                                                                                                                                                                                                                                                                                                                                      /strain="1854"
                                                                                                                                                                                                                                                                                                                                                                                       /organism="Vibrio cholerae"
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                                                                                                                                                                                                      transl_table=11
                                                                                                                                                                                                                         codon_start=1
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                                                                                                                                                                                                                                                                                ctxA"
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ne and ctxB
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gene for cholera
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AUTHORS
TITLE
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ORIGIN
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SOURCE
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LOCUS VCTOXAB56
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TITLE
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                                                                                         -10_signal
                                                                                                             -35_signal
                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 AAGAGGAACTCAGACGGGATTTGTTAGG 325
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                                                                                                                                                                                                                                                                                                               Dams, E., De Wolf, M. and Dierick, W. Nucleotide sequence analysis of the CT operon of cholerae classical strain 569B
                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (25-MAR-1991) E. Dams, Laboratory of Human Biochemistry, RUCA University Antwerp, Gruenenburgerlaan 171, B-2020 Antwerp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholerae.
Vibrio cholerae
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V.cholerae genes for toxin
X58785 S55782
X58785.1 GI:48888
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                                                                                                                                              /organism="Vibrio cholerae"
/strain="classical strain 569
/db_xref="taxon:666"
/clone="pJM17"
72 .127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MIKLKEGVEFTVLLSSAYAHGTPQNITDLCAEYHNTQIYTLNDK
IFSYTESLAGKREMAIITFKNGAIFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTEAK
VEKLCVWNNKTPHAIAAISMAN"
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883. .1257
/codon_start=1
/transl_table=11
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                                                                                                             /rpt_type=TANDEM
145. .156
                                                                                                                                                                                                                                            Location/Qualifiers
1, .1397
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1.000
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/codon_start=1
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                                                                             . 980
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Gaps:
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BCT 30-JUN-1993 569B.

the Vibrio

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AUTHORS
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SOURCE
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LOCUS VCCTX
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Ratio: 1.000
Percent Similarity: 100.000
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CDS
                 misc_feature
                                                 misc_feature
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mat_peptide
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                                                                                                                                                                                                     Cholera toxin genes: nucleotide sequence, vaccine development
                                                                                                                                                                                                                                                                                                         Vibrio cholerae.
Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                           overlapping genes; signal peptide; tandem repeat.
                                                                                                                                                                                                                                                1 (bases 1 to 2020)
Mekalanos, J.J., Swartz, D.J., Pearson, G.D., Harford, N., Groyne, F.
                                                                                                                                                                       84068199
                                                                                                                                                                                                                                           and de Wilde, M.
                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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                   /note="t
                                                                                 /organism="Vibrio cholerae"
/db_xref="taxon:666"
419. .425
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RGYRDRYYSNLDIAPAADGYGLAGFPPEHRAMREEPWIHHAPPGCGNAPRSSMSNTCD
                                                                                                                                                     Location/Qualifiers
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207 c 281 g 449
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                                                                     /note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-"cholera toxin B protein (CTB)"
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/transl_table=11
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                                                                 tandem repetitive sequence"
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VERSION
KEYWORDS
SOURCE
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Quality:
                                                                       seq_documentation_block:
LOCUS E03512
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US-09-528-682-1 x VCCTX
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ORIGIN
                                                                                                               seq_name:
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                                                                                                             gb_pat:E03512
E03512.1 GI:2171728
JP 1992099488-A/17.
synthetic construct.
                                          Cholera toxin gene. E03512
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483. .489
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1289. .1663
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RGYRDRYYSNLDIAPAADGYGLAGFPPEHRAMREEPWIHHAPPGCGNAPRSSISNTCD
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/db_xref="GI:48348"
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|289. .1663
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|gene="ctx B"
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ORIGIN
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LOCUS AF175708
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Ratio: 1.000
Percent Similarity: 100.000
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TITLE
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JOURNAL
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PN JP 1992099488-A/17
PD 31-MAR-1992
PF 20-AUG-1990 JP 1990219523
PF SHIRAI HIROMASA
PI SHIRAI HIROMASA
PC C12M15/11, C1201/68;
CC strandedness: Double;
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3480 bp DNA linear BCT 15-NOV-19 Vibrio cholerae accessory cholera enterotoxin (ace), zonular occludens toxin (zot), cholera enterotoxin A-subunit (ctxA), and cholera enterotoxin B-subunit (ctxB) genes, complete cds. AFI/5708
                                                                                                                                                                 1 (bases 1 to 3480)
Shin, H.J., Park, Y.C. and Kim, Y.C.
Cloning and nucleotide sequence analysis of the virulence gene cassette from Vibrio cholerae KNIH002 isolated in Korea Misainmurhag Hoiji 35 (3), 205-210 (1999)
2 (bases 1 to 3480)
Shin, H.J., Park, Y.C. and Kim, Y.C.
                                                                                                                                                                                                                                                                                                                          Vibrio cholerae.
Vibrio cholerae
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                                                                                                                           Direct Submission
Submitted (04-AUG-1999)
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                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                               University, Kaesin-Dong
                                                                                                                                                                                                                                                                                                                                                                                   AF175708.1 GI:5764645
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                                                                                              Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note='cholera toxin Location/Qualifiers
/organism="Vibrio cholerae"
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Gaps: 0
Percent Identity: 100.000
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                                                                                                             School of Life Sciences, Chungbuk National san 48, Cheongju, Chungbuk-Do 361-763,
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US-09-528-682-1 x AF175708
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ORIGIN
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VEKLCYWNNKTPHAIAAISMAN"
721 c 808 g 1003 t
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/gene="ctxA"
1872. .2648
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nrafyglgaretltyhdaansgomsshaltrovkkipspirkmyastttgkardtmag
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574. .1773
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/transl_table=11
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/transl_table=11
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Bhattacharyyaa,T., Nandy,R.K. and Nair,G.B.
The entire core region of the ctx-phi (ctx-prophage) in VCE 232, an
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4 (bases 1, to 10646)
4 (bases 1, to 10646)
4 (bases 1, to 10646)
5 (bases 1, to 10646)
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1 (bases 1 to 10646)

1 (bases 1 to 10646)

Heidelberg, J. F., Elsen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L., Edill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C. and White, O.
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Vibrio cholerae
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                                                                                                                             Submitted (14-JUN-2000) The Institute for Genomic Medical Center Dr. Rockville, MD 20850, USA Location/Qualifiers
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DNA sequence of both chromosomes of the cholera pathogen Vibrio
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                                                                                        1. .10646
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: Identity:
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/note="similarified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="biotype: El Tor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /serotype="01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INESFEVGSRESRIYWRIYNKAAQLGLDMHWFRNEVELKDMPIDVLLNIEGYFAGLCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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complement (5762. .7045)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAKYLKMDVSDISIEFIDTDHPDGRLTMARFWHWARKDAFLFIDECGRIWPPRLTVTN LKALDTPPDLVAEDRPESFEVAFDMHRHHGWDICLTTPNIAKVHMIREAAEIGYRHF NRATVGLGAKFILTTHDAANSGOMDSHALTRQVKKIPSPIFKMYASTTTGKARDTMAG TALWKORKILFLEGMVFLMESYSFYGLHDNPIFTGGNDATIESEGQSEDGSKATVGNAV GSKAVAPASFGFCIGRLCVQDGFVTVGDERYKLVDNLDIPYRGLMATGHHIYKDTLTV
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VEKLCVWNNKTPHAIAAISMAN"
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/protein_id="AAF94614.1"
/db_xref="GI:9655958"
                                    SNPERCQFPIREAETELETAQQNLKQMINEKITQSALHQFKGSAAVPSFCSYVEAFGY
NLCFDFSLFSENLHIIRMIVLAMAYILAAMLILFR"
                                                                                                                           SLGGTVVPPNPDQPNPTPPDSSSPNYTGALNTISKKLNTLETISQQLDTMNTALSGRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'protein_id="AAF94616.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to SP:P38441 GB:Z22569 PID:298062; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MSIFIHHGAPGSYKTSGALWLRLLPAIKSGRHIITNVRGLNLER/
.7304)
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Ratio: 1.000
Percent Similarity: 100.000
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                                            Percent Similarity: 100.000
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Escherichia coli DNA.
Escherichia coli Escherichia coli Bacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ECOBLINA 165 bp DNA linear BCT 26-APR E.coli heat labile enterotoxin subunit a gene; al/a2 junction. K00433
                                                                                                                                                                                                                                                     1 (bases 1 to 165)
Spicer,E.K., Kavanaugh,W.M., Dallas,W.S., Falkow,S.,
Konigsberg,W.H. and Schafer,D.E.
Sequence homologies between a subunits of Escherichia
Vibrio cholerae enterotoxins
Proc. Natl. Acad. Sci. U.S.A. 78, 50-54 (1981)
                                                                                                                                                                                                                                                                                                                                                                                                                             K00433.1 GI:145829
                                                                        Quality:
                                                                                                                                      about
                                                                                                                                                                                                            see other loci beginning <ecoelt>
                                                            Ratio:
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t 300 bp
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similarity; putative"
/codon_start=1
                                                          24.00
                                                                                                                                   /db_xref="taxon:562"
30 c 35 g
bp after seg 1.
                                                                                                                                                                                                  1. .165
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/gene="VC1462"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MESSLKNKLNTFKSTLSLGVFLLFSAFANQALAAADAGLVTEVTKTLGTSKDTVIALGPLIMGVVGAIVLIVTVIGLIRKAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="colonization factor"
/protein_id="AAF94618.1"
/db_xref="GI:9655962"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="VC1461"
/note="similar to ;
                                                                                                                                                                                 ∕organism≔"Escherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="RstB2 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 (bases 190 to 774)
Yamamoto,T. and Yokota,T.
Sequence of heat-labile enterotoxin of Escherichia for humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto, T., Tamura, T., Yokota, T. and Takano, T. Overlapping genes in the heat-labile enterotoxin from Escherichia coli human strain Mol. Gen. Genet. 188 (2), 356-359 (1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto,T., Tamura,T., Ryoji,M., Kaji,A., Yokota,T. and Takano, Sequence analysis of the heat-labile enterotoxin subunit B gene originating in human enterotoxigenic Escherichia coli J. Bacteriol. 152 (1), 506-509 (1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E.coli heat labile enterotoxin gene, complete cds.
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Escherichia coli
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   Location/Qualifiers
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                                                                                                                                                                          /gene="toxB"
205. .267
                                            /transl_table=11
/product="enterotoxin B"
/protein_id="AAB02982.1"
/db_xref="GI:1395122"
/translation="MNKVKCYVLFTALLSSLCAYGAPQSITELCSEYRNTQIYTINDK
ILSYTESMAGKREMVIITFKSGATFQVEVPGSQHIDSQKKAIERMKDTLRITYLTETK
IDKLCVWNNKTPNSIAAISMEN"
                                                                                                                                                                                                                /gene=
195. .!
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195. .197
                                                                                                                                                                                                                                                                             /codon_start=2
/trans1_table=11
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/translation="AWREEPWIHHAPQGCGDSSRTITGDTCNEETQNLSTIYLRKYQS
                                                                                                                                                                                                                                                                                                                                                                                           /specific_host="Homo sapiens"
/db_xref="taxon:562"
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Escherichia coli"
/strain="H10407"
                                                                                                                                                             'gene="toxB"
                                                                                                                codon_start=1
                                                                                                                               'gene="toxB"
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                                                                                                                                                                                                                              "toxB",
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US-09-528-682-1 x ECOELT
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US-09-528-682-1 x ECOPHLEG5
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LOCUS ECOPHLEG5
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Ratio: 1.000
Percent Similarity: 100.000
                                                         Align seg 1/1 to: ECOPHLEG5
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TyrGlnSerLysValLysArgGlnIlePheSerAspTyrGlnSerGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                              interotoxin in Escherichia coli
Unpublished (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E.coli, DNA.
Escherichia coli
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                                                                                                                            : 22.00
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                                                                                                                                                                                                                              /product="heat-labile enterotoxin"
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/protein_id="AAA2435.1"
/db_xref="GI:147191"
/tzanslation="MKNITFIFFILLASPLYANGDRLYRADSRPPDEIKRSGGL"
213 c 181 g 279 t
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781. .>900
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142 c 153 g
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/transl_table=11
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/strain="K-12"
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Gaps: 0
Percent Identity: 100.000
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LOCUS VIBCTA2
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LOCUS VIBCTA1
              alignment_scores:
                                                                                                                            FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
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ACCESSION
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                                                                                                                                                                                                                                                                                               ACCESSION
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                                                                                                                                         JOURNAL
MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                            199 TTATATCGGGCAGATTCTAGACCTCCTGATGAAATAAAG 237
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                                                                                                                                                                                                                                                                                                                                                                                                                         5 LeuTyrArgAlaAspSerArgProProAspGluIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SArgSerGlyGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio. 1 (bases 1 to 251)
Gennaro, M.L. and Greenaway, P.J.
Nucleotide sequences within the cholera toxin operon
                                                                                                                                                                                                                                                                                                           Vibrio cholerae cholera toxin subunit B 5' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clean copy provided by authors.
Location/Qualifiers
1. .255
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Nucleotide sequences within the cholera toxin operon
Nucleic Acids Res. 11, 3855-3861 (1983)
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1 of 2
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J01846
Quality:
                                                                                                                                                                                                                        Vibrio cholerae (strain El Tor 1621) DNA
Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio cholerae (strain El Tor 1621) DNA
Vibrio cholerae
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                                                                                                                                                                                                                                                                   cholera toxin.
                                                                                                                                                                                                                                                                                J01847.1 GI:155157
                                                                                                                                                                                                                                                                                               J01847
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1 (bases 1 to 255)
                                                                                                                                                      Nucleic Acids Res. 11, 3855-3861 (1983)
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1.000
100.000
                                                                  /organism="Vibrio cholerae"
/db_xref="taxon:666"
38 c 38 g 79 t
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/db_xref="taxon:666"
23 c 38 g 109 t
                                                                                                                         Location/Qualifiers
                                                                                                               1. .251
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subunit A alpha-chain
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-chain 3' end &
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5' end.
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Length:

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KEYWORDS
SOURCE
ORGANISM
                alignment_block:
                                                                                  alignment_scores:
Quality:
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AUTHORS
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VERSION
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ORIGIN
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US-09-528-682-1 x VIBCTA2
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LOCUS VIBTOX
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                                            Quality: 12.00
Ratio: 1.000
Percent Similarity: 100.000
US-09-528-682-1 x VIBTOX
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Percent Similarity:
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The termination codon of subunit A2 overlaps the initiation codon of subunit B by 4 bp. The correct translation of the 2 subunits is the result of a shift in reading frames at this junction. Previous protein structural analysis has shown that the A2 subunit is bound to a precursor of the A subunit. Therefore, the 'met' at position 1 is not an initiator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enterotoxin.

Vibrio cholerae (El Tor biotype strain 62746) DNA, clone pCVD002.

Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholerae toxA and
                                                                                                                                                       188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cholerae enterotoxin
J. Biol. Chem. 258, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; proteobacteria; gamma subdivision; Vibrionaceae; Vibrio. 1 (bases 1 to 512)
Lockman, H. and Kaper, J.B.
Nucleotide sequence analysis of the A2 and B subunits of Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subunits A2 (gamma) and B. K01170
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bp 1
                                                                                                                                                   /product="enterotoxin subunit B mature peptide" ) a 74~c 88~g 151~t upstream of NdeI site.
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                                                                                                                                                                                                           /note="
                                                                                                                                                                                                                                                        /translation="miklkfgyfftvllssayahgtponttdlcaeyhntoiytlndk
Ifsyteslagkremaiitfkngaifqyevpgsohidsokkaiermkdtlriaylteak
Veklcymnnktphaiaaisman"
                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MSNTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDTHNRIKD
EL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAA27572.1"
/db_xref="GI:155297"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Vibrio cholerae"
/db_xref="taxon:666"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                            /protein_id="AAA27573.1"
/db_xref="GI:155298"
                                                                                                                                                                                                                                                                                                                                            /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                /note="enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="enterotoxin subunit
                                                                                                                                                                                                                                                                                                                                                                /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transl_table=11
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                                                                                                                                                                                                                       enterotoxin subunit B signal peptide"
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                                                Length:
Gaps:
Percent Identity:
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Percent Identity:
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AUTHORS
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ORGANISM
              ORIGIN
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                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
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MEDLINE
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                                                                                                  old_sequence
                                                                                                                                                                   old_sequence
                                                                                                                                                                                                                                    old_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M17873 J01605
M17873.1 GI:145832
eltB gene; enterotoxin.
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                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence comparison between heat-labile toxin B-subunit cistrons from Escherichia coli of human and porcine origin Infect. Immun. 48 (1), 73-77 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence homology between coli heat-labile toxin Nature 288 (5790), 499-501 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli DNA.
Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A long inverted repeat which could be a termination signal located at positions 533-564.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia.
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            bp upstream of EcoRI site.
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ong,J., Vinal,A.C. and Dallas,W.S.
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                                225 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Escherichia coli"
/specific_host="Sus scrofa"
/db_xref="taxon:562"
33. .407
                              /citation=[1]
112 c
                                                                                                                                                                     /citation=[1]
223
                                                                                                                                                                                                                                      /product="enterotoxin"
114
                                                                                                                                                                                                                                                                                                                         /translation="MNKVKCYVLFTALLSSLYAHGAPQTITELCSEYRNTQIYTINDK
ILSYTESMAGKREMVIITFKSGETFQVEVPGSQHIDSQKKAIERMKDTLRITYLTETK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene-"eltB"
33. .407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="eltB"
33. .95
                                                              /gene="eltB"
/note="Nature 288,
                                                                                                  /citation=[1]
362
                                                                                                                             /gene="eltB"
/note="Nature
                                                                                                                                                                                                                                                                                                                                                         /product="enterotoxin"
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/db_xref="GI:145833"
                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                          IDKLCVWNNKTPNSIAAISMKN"
                                                                                                                                                                                                     note≖"Nature
                                                                                                                                                                                                                      ′gene="eltB"
                                                                                                                                                                                                                                                                      'gene="eltB"
                                                                                                                                                                                                                                                                                                                                                                                                                                               note="precursor"
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and Escherichia

BCT 16-APR-1996

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REFERENCE
AUTHORS
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ORGANISM
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US-09-528-682-1 x ECOELTBP
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                             sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cloning, nucleotide sequence, and hybridization IIb heat-labile enterotoxin gene of Escherichia J. Bacteriol. 171 (9), 4945-4952 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT-IIb gene; enterotoxin type IIb. Escherichia coli (strain 41) DNA. Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ECOETOXHL 1262 bp DNA linear Escherichia coli (strain 41) heat-labile enterotoxin (LT-IIb) A and B chain genes, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pickett, C.L., Twiddy, E.M., Coker, C. and Holmes, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M28523.1 GI:576584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28, 1994 this sequence version replaced gi:341953 Location/Qualifiers
                                                                                                                                                                                                                         /translation="MAKVISFFISLFLISFPLYANDYFRADSRTPDEVRRSGGLIPRG
QDEAYEGTPINILYDHARGTATGNTRYNDGYVSTTTTLRQAHLLGQNNLIGGYNEYY
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SLTNKLSQHDLADFKKYIKRKFTLMTLLSINNDGFFSNNGGKDEL"
                                                                                                               /product="enterotoxin"
894. .962
                                                                                                                                                                                                                                                                                                                                                                                                                           /gene=
                                                                                                                                                                             /gene="LT-IIb"
173. .901
                                                                                                                                                                                                                                                                                                        /product="enterotoxin"
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             /transl_table=11
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/codon_start=1
                                                                                              /gene≖"
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                                                                                                                                                                                                                                                                                                                                                         transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                         /gene="LT-IIb"
/note="A chain of heat-labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="LT-IIb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="LT-IIb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="pCP4185"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:562"
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                                                                                            "dil-II
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                                               type
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ORIGIN
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US-09-528-682-1 x AR019034
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LOCUS A69697
                                                                                                                                          seq_name: gb_pat:A69697
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/translation="mgfkkiikafvimaalvsvqahagasqffkdncnrttaslvegv
ELTKYISDINNNTDGMYVVSSTGGVWRISRAKDYPDNVMTAEMRKIAMAAVLSGMRVN
MCASPASSPNVIWAIELEAE"
/note="B chain of heat-labile enterotoxin type IIb"
/product="enterotoxin"
, 195 c 285 g 413 t
                                                                                                              963. .1259
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alignment_block:
US-09-528-682-1 x ECOETOXHL
                                                       Align seg 1/1 to: ECOETOXHL
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Ratio: 1.000
Percent Similarity: 100.000
278 AACATTAACCTATATGACCATGCACGAGGTACT 310
            38 AsnIleAsnLeuTyrAspHisAlaArgGlyThr 48
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: Identity:
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100.000
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1 (bases 1 to 42)
NOTiega,F.R. and Levine,M.M.
Notinga,F.R. and Levine,M.M.
Gua mutants of shigella spp. and vaccines containing the same Patent: US 5783196-A 14 21-JUL-1998;
                                                                                                                                                                                                                                                    Sequence 14 from patent US AR019034
                                                                                                                                                      Unclassified
                                                                                                                                                                                                                                    AR019034.1 GI:3974148
/organism="unknown"
8 c 10 g
                                                         Location/Qualifiers
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5 5783196.
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Length: Gaps: Percent Identity:

10 0 100.000

Align seg 1/1 to: AR019034 from: . : 42

192 ArgThrIleThrGlyAspThrCysAsnGlu AGAACAATTACAGGTGATACTTGTAATGAG 201 42

2724 bp Sequence 15 from Patent WO9807864 A69697 unidentified unidentified A69697.1 GI:4774310 DNA linear PAT 07-MAY-1999

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REFERENCE
AUTHORS
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Ratio: 1.000
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                          Shone,C.C., Quinn,C.P. and Foster,K.A.
Recombinant toxin fragments
Patent: JP 2001502890-A 8 06-MAR-2001;
MICROBIOLOGICAL RESEARCH AUTHORITY CAMR,THE SPEYWOOD LABORATORY LTD
OS Unidentified
PN JP 2001502890-A/8
PD 06-MAR-2001
PF 22-AUG-1997 JP 1998510524
PR 23-AUG-1996 GB 9617671.4,13-DEC-1996 GB 9625996.5 PI
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1 (bases 1 to 2724)

1 (bases 1 to 2724)

FOSTET.K.A., Quinn,C.P. and Shone,C.(
RECOMBINANT TOXIN FRAGMENTS

Patent: WO 9807864-A 15 26-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
PF 22-AUG-1997 JP 1998510524
PR 23-AUG-1996 GB 9617671.4,13-DEC-1996 GB 9625996.5 PI
CLIFFORD CHARLES SHONE, CONRAD PADRAIG QUINN, KEITH ALAN FOSTER PC
                                                                                                                                                                                                                                                                                       unidentified
                                                                                                                                                                                                                                                                                                            unidentified.
                                                                                                                                                                                                                                                                                                                                  BD009884.1 GI:18638257 JP 2001502890-A/8.
                                                                                                                                                                                                                                                              unclassified.
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                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant toxin fragments.
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                                                                                                                                                                                                                               (bases 1 to 2724)
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LQENEERLYYYKKFKDLASTLNKAKSIVGTTASLQYMKRVFKEXYLLSEDTSGKESVD
KLKEDKLYKMLTEIYEDNFVKFEKULNKTYLLNEDKAVFKINIVPKVNYTIVOGFU
RNTNLAANFNGQNTEINNMNFTKLKNFTGLFEFYKLLCVRGIITSKTKSLDKGYNKIE
RRUNLAANFNGQNTEINNMNFTKLKNFTGLFEFYKLLCVRGIITSKTKSLDKGYNKIE
GRCDGALNDLCIKVNNWDLFFSDSEDNFUDLNKGEEITSDTNLEAAEENISLDLIQQ
YYLTRNFDUBPENISLENLSSDIIGOLELMPNIERFFYKKYELDKYTMFHYLRAQEE
EHGKSRIALINSVNEALLNPSRVYTFFSSDYVKKVNKATEAAMFLGWVEQLVYDFTDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSEVSTTDKIADITIIIPYIGPALNIGNMLYKDDFVGALIFSGAVILLEFIPEIAIPY
LGTFALVSYIANKVLTVQTIDNALSKRNEKWDEVYKYIVTNWLAKVNTQIDLIRKKMK
EALENQAEATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESINKAMININKFLNQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVSYLMNSMIPYGVKRLEDFDASLKDALLKYIYDNRGTLIGQVDRLKDKVNNTLSTDI
PFQLSKYVDNQRLLSTFTEYIKSRPQSKVKRQIFSGYQSDIDTHNRIKDEL"
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LGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDGSYRSEELNLVIIGPSADI
IQFECKSFGHEVLNLTRNGYGSTQYIRFSPDFTFGFEESLEVDTNPLLGAGKFATDPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAB42522.1"
/db_xref="GI:4774311"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="unnamed protein product"
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US-09-528-682-1 x BD009884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154611 bp DNA linear HTG 30-HOMO sapiens chromosome 10 clone RP11-283C16, WORKING DRAFT SEQUENCE, 15 unordered pieces.
                                                                                                                                                                                                                                                                                                        Street, Waltham, MA 02453, USA
On Apr 27, 2001 this sequence version replaced g1:11545931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                               Submitted (11-MAY-2000) Genome Therapeutics Corporation, 100 Beaver
                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Therapeutics Corporation Sequencing Center: Human Genome
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                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                      Smith, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Data
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/db_xref="taxon:32644"
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Sequencing vector: N/A
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 990315
Consensus quality: 167668 bases at least Q40
Consensus quality: 171341 bases at least Q30
Consensus quality: 173207 bases at least Q20
Insert size: 177782; sum-of-contigs
Quality coverage: 6.1x in Q20 bases; sum-of-contigs
                                                                                                                                                   Center: Genome Therapeutics Corporation Center code: GTC Web site: http://www.genomecorp.com/
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* NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown

exact sizes of the gaps are unknown

HTG 30-AUG-2001

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BASE COUNT
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124121. .154611
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94216. .124020
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11348. .14041
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33993: contig
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AUTHORS
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US-09-528-682-1 x AC068893/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-JAN-2000) Genome Therapeutics Corporation, 1 Street, Waltham, MA 02453, USA On Apr 28, 2001 this sequence version replaced gi:9937742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC021033 166872 bp DNA linear HTG 30-
Homo sapiens chromosome 10 clone RP11-310A17, WORKING DRAFT
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                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently 
* consists of 24 contigs. The true order of the pieces 
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Data
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                                                                                                                                                                    * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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                            1139: contig of 1139 bp in length
1239: gap of unknown length
2468: contig of 1229 bp in length
2568: gap of unknown length
3970: contig of 1402 bp in length
4070: gap of unknown length
5550: contig of 1480 bp in length
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                                                                                                                                                                                                                                                                       Sequencing vector: N/A
Sequencing vector: N/A
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 990315
Consensus quality: 181482 bases at least Q30
Consensus quality: 184094 bases at least Q30
Consensus quality: 185257 bases at least Q20
Insert size: 191465; sum-of-contigs
Quality coverage: 6.3x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: gtc-seqcenter@genomecorp.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Genome Therapeutics Corporation Center code: GTC
                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.genomecorp.com/
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clone_end:SP6"
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                            /note="assembly_name:Contig23"
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17550. .20361
                                                                                                                                                                                                            'note=
                                                                                                                                                                                                                                        'note='
                                                                                                                                                                                                                                                                                                  note="assembly_name:Contigl3"
                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                           'note="assembly_name:Contig1"
                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RP11-310A17"
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149761: 0
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_11095
                                                                                                                                                                                                                                                                                                                  "assembly_name:Contigl1"
.5550
                                                                                                                                                                                                                                                                                                                                                  .3970
                                                                                                                                                                                                                                                                                                                                                                                . 2468
                                                                                                                                                                                                                                       assembly_name:Contig15"
                                                                                                                                                                                                                                                                                       . 6874
                                                                                                                                                                                                                                                                     assembly_name:Contigl4"
                                                                                                                                                                                                                                                                                                                                                             assembly_name:Contig9"
                                                          .24773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5: gap of unknown length
6: contig of 5451 bp in length
6: gap of unknown length
1: contig of 7855 bp in length
1: contig of 7855 bp in length
1: contig of 7855 bp in length
1: contig of 6667 bp in length
1: gap of unknown length
1: gap of unknown length
1: gap of unknown length
9: contig of 8358 bp in length
9: gap of unknown length
9: contig of 11620 bp in length
9: contig of 11620 bp in length
9: contig of 71620 bp in length
1: contig of 12555 bp in length
4: contig of 7841 bp in length
5: contig of 2850 bp in length
5: contig of 29850 bp in length
5: gap of unknown length
1: contig of 78156 bp in length
1: gap of unknown length
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of 2812
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of 1056
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of 1639
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TITLE
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ORGANISM
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LOCUS AC073367
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US-09-528-682-1 x AC021033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_pr:AC073367
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                                                               FEATURES
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                             TITLE
JOURNAL
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Ratio:
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                                                             Direct Submission
Submitted (25-0CT-2001) Genome Therapeutics Corporation, 100
Street, Waltham, MA 02453, USA
On Oct 25, 2001 this sequence version replaced gl:15553107.
Location/Qualifiers
                                                                                                                                                          Direct Submission
Submitted (15-JUN-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA
3 (bases 1 to 168918)
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 168918)
Smith, D.R.
                                                                                                                                             Smith, D.R.
                                                                                                                                                                                                                        2 (bases 1 to 168918)
Smith, D.R.
                                                                                                                                                                                                                                                                          Sequence Data
                                                                                                                                                                                                                                                                                         Genome Therapeutics Corporation Sequencing Center:
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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clone_end:T7"
34617. .42471
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48045, .54711
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/note="assembly_name:Contig26"
42572. .47944
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/db_xref="taxon:9606"
/chromosome="10"
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149762. .166872
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34417 c 33394 g 49026 t
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54812. .63169
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74990. .87514
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                                                   .168918
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Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                          Human Genome
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                                                                                                               Beaver
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BASE COUNT ORIGIN /clone="RP11-197M22" /clone_lib="RPCI-11" 49033 a 34070 c 34897 g 50918 t

alignment_scores: 10.00 Length: 10 Quality: 10.00 Length: 10 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block: US-09-528-682-1 x AC073367/rev ...

Align seg 1/1 to reverse of: AC073367 from: 1 to: 168918

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-(q-/cgln2_1/USPTO_spco1/US09528682/runat_18062002_082606_8842/app_query.fasta_1.299
-DB=N_Geneseq_032802 -CpmT-fastap -SUFFIX=011p2n.rng
-GAPOP=4.500 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -GAPEXT=0.050 -GAPEXT=7.000 -YGAPOP=60.000
-YGAPEXT=60.000 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000
-YGAPEXT=60.000 -FGAPOP=6.000 -FGAPEXT=7.000 -START=1
-MATRIX=011g0 -TRANS=human40.cdi -LIST=1000 -DOCALIGN=200
-THR_SCORE=quality -THR_MIN=1 -ALIGN=50 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MAINLEND -MATRIX=00000000
-USER=-US09528682_CGN1_1_563 -NCPU=6 -TOPU=3 -LONGLOG
-USER=-US09528682_CGN1_1563 -NCPU=6 -TOPU=3 -LONGLOG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          time
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/SIDS5/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:AAK21762 - 7
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/SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAK44046 + 7
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/SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAK455337 - 7
/SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAK455337 - 7
/SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAK455337 - 7
/SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAK55337 - 7
/SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAK55337 - 7
/SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAK45046 + 7
/SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAK55337 - 7
                                                                                                  alignment_scores:
Quality:
Ratio:
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US-09-528-682-1 x AAN50205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name:
Align seg
                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _documentation_block:
                                                                                                                                                                                                                            AAN50205 is the gene sequence of the natural LTA gene. The LTA gene the site directed mutant SDM1 (see AAN50206) is inactive. The inventors claim a vaccine prepr. active against pig scours which contains an inactivated LTA component, together with additional K88 antigens opt. with whole cells comprising the antigens or contg. the inactivated LTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP145486-A
                                                                                                                                                                                              Sequence 777
                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                          New toxoid as inactivated form of toxin obtd. from organism transformed by gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-DEC-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-DEC-1984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1985-148358/25
1/1
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ţo:
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                                                                                                                                                                                              BP;
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AAN50205
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<u>ب</u>
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Gaps:
Identity:
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4.5e+03

7.5e+03

7.5e+03

4.5e+03

4.5e+03
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08-OCT-1992

(first entry)

LTh; STla; probe; dete

detection;

SS

ST1b; thermolabile;

heat-stable;

E.coli;

T4DNA ligase;

Thermolabile toxin (LTh) gene

seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:AAQ23864

_documentation_block:

AAQ23864

standard;

DNA;

1148 BP

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167
                                       705
                                                         217
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snArgIleArgAspGluLeu 240
|||||||||||||||||||
|ACAGAATTCGGGATGAATTA 774
                                                                                                                                                                                           yrIleTyrVall1eAlaThrAlaProAsnMetPheAsnValAsnAspVal
                                                                                                                                                                                                                                                                                                                                                                                   sValLysArgGlnIlePheSerAspTyrGlnSerGluValAspIleTyrA
                                                                                      GluGluThrGlnAsnLeuSerThrIleTyrLeuArgGluTyrGlnSerLy
                                                                                                                   CACAAGGTTGTGGAAATTCATCAAGAACAATCACAGGTGATACTTGTAAT
                                                                                                                            roGlnGlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn
                                                                                                                                                       yGlyIleProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyV
                                                                                                                                                                                                                                                                                                                     LeuGlyValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sArgSerGlyGlyLeuMetProArgGlyHisAsnGluTyrPheAspArgG
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                                                                             TTAGGCGTATACAGCCCTCACCCATATGAACAGGAGGTTTCTGCGTTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACGTTCCGGAGGTCTTATGCCCAGAGGGCATAATGAGTACTTCGATAGAG
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                                       AGTTAAGAGGCAGATATTTTCAGACTATCAGTCAGAGGTTGACATATATA
                                                                                                                                                                                                                                                                       TGGAATACCATATTCTCAGATATATGGATGGTATCGTGTTAATTTTGGTG
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alignment_block:
US-09-528-682-1 x AAQ23864
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                                                                                                                                                                                                                                                                                                                                                                                                                  Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The thermolabile toxin (LTh) gene sequence is derived from enterotoxigenic E. coli. An LTh-STla-STlb probe, wherein all all or part of the sequences of the three toxin genes represented in AAQ23864-66 are ligated to each other by T4DNA ligase, may be used for the detection of Vibrio cholerae and enterotoxigenic E.coli Simultaneously in a simple way.

The method has the same sensitivity as the dangerous radio-isotope
                      121
                                            367
                                                                 105
                                                                                       317
                                                                                                                                 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-137930/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KITA ) KITASATO RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 208.00
Ratio: 1.000
Similarity: 100.000
                                                                                     uAlaGlyGlnSerIleLeuSerGlyTyrSerThrTyrTyrIleTyrValI 88
                                                                                                                                                                                                                                                                                 yLeuMetProArgGlyHisAsnGluTyrPheAspArgGlyThrGlnMetA 38
                                                                                                                                                                                                                                                                                                                           LeuTyrArgAlaAspSerArgProProAspGluIleLysArgSerGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and RNA probe - for simultaneous detection entero-toxigenic E. coli
          rSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyValIleAspGluA 138
                                                      SerProHisProTyrGluGlnGluValSerAlaLeuGlyGlyIleProTy 121
                                                                                                                                                                                                                                                                                                               TTATACCGTGCTGACTCTAGACCCCCAGATGAAATAAAACGTTCCGGAGG
AGCCCTCACCCATATGAACAGGAGGTTTCTGCGTTAGGTGGAATACCATA
                                                                                                                                                                                                                                                                    TCTTATGCCCAGAGGGCATAATGAGTACTTCGATAGAGGAACTCAAATGA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 1; 15pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90JP-0194208
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Gaps: 0
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466
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seq_documentation_block:
ID AAA51106 standard;
seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138
                                                                                                                                                                                                                                                  sig_peptide
                                                                                                                                                                                                                                                                                                                           adjuvant;
                                              New polynucleotides encoding LT-A or CT-J
transformation of plant cells, useful in
elicit immune responses in animals
                                                                                WPI; 2000-442653/38.
P-PSDB; AAY96646.
                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                                                    Plant-optimized E.
                              Example 1; Fig 1; 103pp; English.
                                                                                                        Mason HS,
                                                                                                                       (BOYC-) BOYCE THOMPSON INST PLANT (MASO/) MASON H S. (ARNT/) ARNTZEN C J.
                                                                                                                                                          22-DEC-1998;
                                                                                                                                                                          22-DEC-1999;
                                                                                                                                                                                           29-JUN-2000
                                                                                                                                                                                                          WO200037609-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnLeuSerThrIleTyrLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sGlnAlaTrpArgGluGluProTrpIleHisHisAlaProGlnGlyCysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProProAspHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAAGCTTGGAGAAGAACCCTGGATTCATCATGCACCACAAGGTTGTG
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                                                                                                                                                                                                                                                                                                                           anti-bacterial;
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                                                                                                                                                                                                                                                                                                           coli.
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3..56
                                                                                                                                                          98US-0113507
                                                                                                                                                                         99WO-US30747
                                                                                                                                                                                                                                   /*tag=
57..779
                                                                                                                                                                                                                                                                           Location/Qualifiers 3..782
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                                                                                                                                                                                                                                                                                                                                                                                                      CDNA;
                                                                                                                                                                                                                                                                                                                                  LT-A; LT-B; mutant;
                                                                                                                                                                                                                                                                                                                                                    coli heat labile toxin A subunit coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                      782
                                                                                                                                                                                                                                                           heat-labile_toxin-A
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                                                       CT-A polypeptides for the 
l in immunogenic compositions
                                                                                                                                                                                                                                                                                                                                   transgenic
                                                                                                                                                                                                                                                                                                                                   plant;
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                                                                                                                                                                                                                                                                                                                                    vaccine; oral;
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This plant-codon optimized cDNA encodes a synthetic Escherichia coli heat-labile toxin (LT) A subunit (LT-A). The sequence contains plant-preferred codons and eliminates sequence motifs associated with

associated with

622

GA 623

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alignment_block:
US-09-528-682-1 x AAA51106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was made to accomodate the creation of a Ncol restriction site around the initiator methionine codon. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the production of transgenic plants for the
               188
                                                                                           171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutant polypeptides are also useful as adjuvants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spurious mRNA processing. A single codon insertion (GTG encoding valine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 LeuTyrArgAlaAspSerArgProProAspGluIleLysArgSerGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity:
                                                                                                                                                                                                                                                                                                       rSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyValIleAspGluA 138
                                                                                                                                                                                                                                                                                                                                                                                  SerProHisProTyrGluGlnGluValSerAlaLeuGlyGlyIleProTy 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                            leAlaThrAlaProAsnMetPheAsnValAsnAspValLeuGlyValTyr 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCAGGACAATCCATCCTCAGGATACTCCACCTACTACATCTATGTGA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uAlaGlyGlnSerIleLeuSerGlyTyrSerThrTyrTyrIleTyrValI 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATGATGATGGATATGTGTCCACCTCCCTTAGCTTGAGGTCTGCTCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrAspAspGlyTyrValSerThrSerLeuSerLeuArgSerAlaHisLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCTATAGGGCTGACTCTAGGCCCCCAGATGAGATCAAGAGGTCTGGAGG
                                                                                                                                                    GGCTCCATAGGAATAGGGAGTATAGGGACAGGTACTATAGGAACCTCAAC
                                                                                                                                                                                                                            rgLeuHisArgAsnArgGluTyrArgAspArgTyrTyrArgAsnLeuAsn 154
                                                                                                                                                                                                                                                                                   TTGCTACAGCACCAAACATGTTCAATGTGAATGATGTGTTGGGAGTGTAT
                                                                                                                                                                                                                                                                                                                                                               AGCCCTCACCCATATGAGCAAGAGGTGTCTGCTTTGGGTGGAATCCCATA 421
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seq_name:
Plant-optimized E. coli LT-A G192 mutant coding sequence
                                                                                                                                               AAA51544 standard; cDNA;
                                                                                                                                                                                                                  /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA51544
                                                (first entry)
                                                                                                                                                  782
```

Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; anti-bacterial; R192G; SS

oral;

/product= /*tag= 60..779 Location/Qualifiers 3..782 /*tag= /*tag= ٥ a a heat-labile_toxin-A

98US-0113507 99WO-US30747

(MASO/) MASON H S. (ARNT/) ARNTZEN C J. BOYCE THOMPSON INST PLANT RES. MASON H S.

Arntzen CJ;

New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions of the composition of plant cells, useful in immunogenic compositions. immune responses in animals compositions 6

Example 3; Page -; 103pp; English.

seq_documentation_block:
ID AAA51544 standard; cD
XX AAA51544;
XC AAA51544;
XX AAA51544;
XX Pant-optimized E. cc
XX Heat-labile toxin; LT
XX Heat-labile toxin; LT
XX Heat-labile toxin; LT
XX Synthetic.

XX Escherichia coli.

OS Synthetic.

XX Synthetic.

XX Synthetic.

XX Heat-labile toxin; LT
XX Adjuvant; anti-bacter
XX Adjuvant; anti-bacter
XX Adjuvant; anti-bacter
XX Adjuvant; anti-bacter
XX Heat-labile toxin; LT
XX Adjuvant; anti-bacter
XX Adjuvant; anti-bacter
XX Hey Synthetic.

XX WO200037609-A2.

XX WPI; 2000-442653/38.

PF 22-DEC-1998; 98US-C
XX WPI; 2000-442653/38.

PF 200-442653/38.

PF 200-442653/38.

PF 200-442653/38.

PF 200-442653/38.

PF 200-442653/38.

PF 200-442653/38.

PF 2000-442653/38.

PF 2000-426648.

XX WPI; 2000-442653/38.

PF 2000-4426 CC processing. A single codon insertion (GTG encoding valine) was made to CC accomodate the creation of a NcoI restriction site around the CC initiator methionine codon. Novel polynucleotides encode a mutant LT-A CC polypeptide or a mutant Vibrio cholera cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to CC the wild-type LT-A or CT-A polypeptide and where at least one of the CC codons is altered to a plant preferred codon. The polynucleotide further CC comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B CS subunit (CT-B). The polynucleotides are useful for the transformation of CT plant cells for the production of transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the prophylactic or therapeutic treatment against E. coli or V. cholerae. CC prophylactic or therapeutic treatment against E. coli or V. cholerae. CC The mutant polypeptides are also useful as adjuvants. CC constructed from the wild type LT-A cDNA shown in AAA51106 which is A subunit (LT-A). The nucleotide at position 631 was changed from the wild-type A to G which causes a change of arginine to glycine in the mature protein at residue 192. The sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA This cDNA encodes a mutant R192G Escherichia coli heat-labile toxin (A subunit (LT-A). The nucleotide at position 631 was changed from the Figure 1 of the specification (E)

```
seq_documentation_block:
ID AAN50206 standard; DN
XX
AC AAN50206;
XX
DT 30-OCT-1991 (first 6
XX
DT Sequence of the pig 6
DE site directed mutant
XX
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Quality:
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US-09-528-682-1 x AAA51544
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                                                                                                                                                                                                       seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:AAN50206
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Ratio: 1.000
Percent Similarity: 100.000
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                   Sequence of the pig scours site directed mutant SDM1.
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                                                                                                                                                                                                                                                                                                                                         sGlnAlaTrpArgGluGluProTrpIleHisHisAlaProGlnGlyCysG
                                                                                                                                                                                                                                                                                                                                                                                                                AGCCCTCACCCATATGAGCAAGAGGTGTCTGCTTTGGGTGGAATCCCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leAlaThrAlaProAsnMetPheAsnValAsnAspValLeuGlyValTyr 104
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Quality:
Ratio:
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US-09-528-682-1 x
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                     145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New toxoid as inactivated form of toxin for use in obtd. from organism transformed by gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAP50191.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-DEC-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-DEC-1984;
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                                                                                                                             rArgValAsnPheGlyValIleAspGluArgLeuHisArgAsnArgGluT
                                                                                                                                                                                                                                                                                                                                                        ACTTCTCTTAGTTTGAGAAGTGCTCACTTAGCAGGACAGTCTATATTATC
                                                        TCGTGTTAATTTTGGTGTGATTGATGAACGATTACATCGTAACAGGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harford S,
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/note= "TCC
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P-PSDB;
The present sequence encodes for Escherichia coli heat-labile enterotoxin (LT) mutant LT563Y. LTS63Y and LTdel110/J12 (AAU00507) are two novel detoxified and immunologically active proteins (LT mutants) derived by site-directed mutagenesis of the Al subunit of
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                                                                                                                       New detoxified mutants of Escherichia coli heat-labile enterotoxin useful as vaccine for preventing and treating diarrhoea, and as ad for antibody production -
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                                                                                          Page 41-42;
                                                                                                                                                                                                                                                     Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e enterotoxin; LT; LTS63Y; LTdell110/112; mutant;
and immunologically active protein; ADP-ribosylation;
diarrhoea; ds.
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/product= "LTS63Y mutant protein"
/transl_except= (pos:938..939,aa:Met)
/note= "This codon has an apparent 1 nucl
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lAspIleTyrAsnArgIleArgAspGluLeu
                                                                                                         spThrCysAsnGluGluThrGlnAsnLeuSerThrIleTyrLeuArgGlu
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Seq_documentation_block:
ID AAS01506 standard; DN
AC AAS01506;
XX AAS01506;
XX AAS01506;
XX E. coli heat-labile enteroto
KW Heat-labile enteroto
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                                                                                                                                                                                                                    are two novel detoxified and immunologically active proteins (IT mutants) derived by site-directed mutagenesis of the Al subunit of wild type IT. The substitution of Ser to Tyr at position 63 in LTS63Y blocks (LTdell10/112 eliminate the enzymatic activity of LT. The Al subunit of wild type LT catalyses ADP-ribosylation of Gs, a GTP-binding protein that regulates cAMP levels. The resulting increase in cAMP is the cause of diarrhoen in humans and animals e.g. pigs. The mucosal immunogenicities of mutant heat-labile endotoxins LTS63Y and LTdell10/112 were tested. Groups of mice were immunised with LTS63Y or LTdell10/112. The control groups received phosphate buffered saline (PBS) alone. The serum and caecal antibody titres to LT were determined. The results showed that comparable level of anti-LT antibodies in sera and faecal extracts compared with those immunised with wild-type LT. The LT mutants are useful as a vaccine for preventing and treating diarrhoea and as an active of antibody production.
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and immunologically active protein; ADP-ribosylation;
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/note= "This codon has an apparent 1 nucleotide
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AC AAA51147;
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XX Plant-optimized E. cc
XX Heat-labile toxin; L7
KW Heat-labile toxin; L7
KW adjuvant; anti-bactes
XX Escherichia coli.
OS Synthetlc.
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Heat-labile toxin; LT-A; LT-B; mutant; adjuvant; anti-bacterial; S63K; ss.
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) MASON H S.
) ARNTZEN C J.
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XX Heat-labile toxin; LT
XX Heat-labile toxin; LT
XX Heat-labile toxin; LT
XX Adjuvant; anti-bacter
XX Escherichia coli.
OS Synthetic.
CDS /*tag
FT CDS /*tag
FT Sig_peptide /*tag
XX WPI; 2000-442653/38.
DR P-SDB; AAY96649.

XX

C (BANT)/) ARNITEN C J.

XX

DR WPI; 2000-442653/38.
DR P-SDB; AAY96649.

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C (BANT)/) ARNITEN C J.

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initiator methionine codon. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible
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                                                                                                                                                                                                                                                                                                                                                                  This CDNA encodes a mutant A72R Escherichia coli heat-labile toxin (LT) A subunit (LT-A). The nucleotides at position 273-274 were changed from the wild-type GC to AG which causes a change of alanine to arginine in the mature protein at residue 72. The sequence contains plant-preferred
                                                                                                                                                                                                                                                             processing. A single codon insertion (GTG encoding valine) was made to accompate the creation of a NcoI restriction site around the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositielicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   599
                                                                                                                                                                                                                                                                                                                                       codons and eliminates sequence motifs associated with spurious mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BOYC-) BOYCE THOMPSON INST PLANT RES. (MASO/) MASON H S. (ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral; adjuvant; anti-bacterial; A72R; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant-optimized E. coli LT-A R72 mutant coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACCATGCACCACAAGGTTGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page -; 103pp; English.
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60..779
/*tag= c
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seq_documentation_block:
ID AAQ51314 standard; DNA; 711 BP
XX
AC AAQ51314;

XX
DT 08-DEC-1993 (first entry)
XX
Encodes Asp-53 E.coli heat lab
XX
enterotoxigenic bacteria; vacc
KW protomer A; site-directed muta
XX
enterotoxigenic bacteria; vacc
KW protomer A; site-directed muta
XX
Encodes Asp-53 E.coli heat lab
XX
EN protomer A; Location/Quali
XX
Escherichia coli.
XX
Escherichia coli.
XX
Encodes Asp-53 E.coli heat lab
XX
ADP-ribosyltransferase activit
XX
FN protomer A; Site-directed muta
XX
ADP-ribosyltransferase activit
XX
FN protomer A;
FN hote= "wild-t
XX
PN WO9313202-A.
XX
PD 08-JUL-1993.
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US-09-528-682-1 x AAA51545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:AAQ51314
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Note: This sequence does not appear in the specification. It was constructed from the wild type LT-A cDNA shown in AAA51106 which is given in Figure 1 of the specification.
                                                                                                                                                                                                                enterotoxigenic bacteria; vaccine; immunogenic protomer A; site-directed mutagenesis; reduced ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           526
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                                                                                                                                                                                                                                                                                            Encodes Asp-53 E.coli heat labile toxin subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 782 BP; 226 A; 185 C; 191 G; 180 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laProAlaGluAspGlyTyrArgLeuAlaGlyPheProProAspHisGln 172

    uHisargasnargGluTyrargaspargTyrTyrargasnLeuasnIlea

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    CCATAGGAATAGGGAGTATAGGGACAGGTACTATAGGAACCTCAACATAG

    525

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rOHisProTyrGluGlnGluValSerAlaLeuGlyGlyIleProTyrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaTrpArgGluGluProTrpIleHisHisAlaProGlnGlyCysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCACCCATATGAGCAAGAGGTGTCTGCTTTGGGTGGAATCCCATACTCC
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Ratio:
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                                                                              /note= "wild-type GTC(Val) mutated
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Gaps: 0
Identity: 100.000
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                                                                                                                                                                                                                                      toxicity;
                                                                                                                                                                                                                                                      detoxified
                                                                                to GAT(Asp)"
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                                                                                                                                                                                                                                                      LT-A;
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seq_documentation_block:
ID    AAQ51315 standard; Dt
XX
AC    AAQ51315;
XX
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                        545
                                                                                                                                                   186
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                                                                                                                                                                                                                                                                                                                                                                                                   119
                                                                                                                                                                                                                                                                                                                                                                                                                                             103 ValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGlyGlyIl 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunogenic, detoxified LT-A proteins and their use in vaccines protect against enterotoxigenic E.coli. Sequence AAQ51314 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino acid numbering is based on the cholera toxin A subunit sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enterotoxin producing Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-227320/28.
P-PSDB; AAR38730.
                                                                                                                                                                                                                                                                                                                                                                                                                               295 GTATACAGCCCTCACCCATATGAACAGGAGGTTTCTGCGTTAGGTGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Fig 2 and Page 46; 60pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 711 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domenighini M, Hol W,
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                                                                                                                                                                                lyCysGly 188
                                                                                                                                                                                                                                             CTGAATATAGCTCCGGCAGAGGATGGTTACAGATTAGCAGGTTTCCCACC
                                                                                                                                                                                                                                                            LeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProPr 169
                                                                                                                                                                                                                                                                                                        ATGAACGATTACATCGTAACAGGGAATATAGAGACCGGTATTACAGAAAT
                                                                                                                                                                                                                                                                                                                        spGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyrArgAsn
                                                                                                                        GTTGTGGA 552
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                                              DNA;
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                                              711 BP
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Gaps:
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic detoxified mutant cholera toxin and heat labile - useful as vaccines against infection by Vibrio cholerae are enterotoxin producing Escherichia coli
                                                        136
                                                                                   345
                                                                                                                                      Claim
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protomer A; site-directed mutagenesis; reduced toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-DEC-1993
                                                                                                                                                                                                                                                                                                                                             Sequence 711 BP; 236 A;
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                                           spGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyrArgAsn
                                                                                ACCATATTCTCAGATATATGGATGGTATCGTGTTAATTTTGGTGTGATTG
                                                                                              eProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyValIleA 136
LeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProPr
                            ATGAACGATTACATCGTAACAGGGAATATAGAGACCGGTATTACAGAAAT
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                                                                                                                                                                                            1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E.coli heat labile toxin subunit A
                                                                                                                                                                                            AAQ51315
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1.000
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/note= "wild-type GTC(Val) mutated
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Gaps:
Percent Identity:
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100.000
                                                                                                                                                                                                                                                                                                                                             0 other;
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                             444
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seq_documentation_block:
ID AAQ51316 standard; DB
AC AAQ51316;
XX
AC AAQ51316;
XX
DT 08-DEC-1993 (first 6
XX
enterotoxigenic bacta
KW protomer A; site-dira
KW protomer A; site-dira
KW ADP-ribosyltransferat
XX
Escherichia coli.
XX

XX
BOP-ribosyltransferat
XX

BOP-ribosyltransferat
XX

BOP-ribosyltransferat
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BOP-ribosyltransferat
XX

BOP-ribosyltransferat
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BOP-ribosyltransferat
XX

BOP-ribosyltransferat
XX

ADP-ribosyltransferat
XX

BOP-1991; 91IT-1993.
XX

ADP-1992; 92WO-1
XX

BOP-1991; 91IT-1
XX

BOP-1991; 91IT-1
XX

BOP-1991; 91IT-1
XX

BOP-PSDB; AAR38732.
XX

DOMENIGHIA M, HOLI
XX

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                                                                                             The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51316 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic detoxified mutant cholera toxin and heat labile tu- useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enterotoxigenic bacteria; vaccine; immunogenic protomer A; site-directed mutagenesis; reduced ADP-ribosyltransferase activity; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 lyCysGly 188
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DB; AAR38732.
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                                                                                                                                                                                                                                                                                                                                                                                                      3; Fig 2 and Page 46; 60pp; English.
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            235
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                                                                       the cholera
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            155
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            G;
               198
                                                                       toxin A subunit sequence)
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            other;
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alignment_scores:
Quali

Percent Similarity:

1.000 1.000 100.000

Percent Identity:

100.000

Gaps:

Ratio:

alignment_block: US-09-528-682-1 x AAQ51316

Align seg

AAQ51316

ç O:

711

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seq_documentation_block:
ID AAQ51317 standard; DN
AC AAQ51317;
AC AAQ51317;

XX AC AAQ51317;

XX BC OBEC-1993 (first & COL;
XX enterotoxigenic bact;
XX enterotoxigenic bact;
XX enterotoxigenic bact;
XX EScherichia coll.
XX ADP -ribosyltransfera;
XX EScherichia coll.
XX ESCHERICHIA coll.
XX BC ESCHERICHIA COLL.
XX ADP -ribosyltransfera;
XX COLL.
XX ADP -ribosyltransfera;
XX BC CBC-191; CLCa
FT misc_difference 184.
FT Misc_difference 184.
FT MISC_192; 92WO-
XX WO9313202-A.
XX DBC-1992; 92WO-
XX ADP -ribosyltransfera;
XX DBC-1991; 91TT-
XX ADP -PSCB-1991; 91TT-
XX ADP -PSCB-1993-227320/28
DR P-PSCB-1993-227320/28
DR 
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                                                                                                              Immunogenic detoxified mutant cholera toxin and leuseful as vaccines against infection by Vibrio enterotoxin producing Escherichia coli
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                                                              Fig 2 and Page 46;
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                                                                                                                                                                                                                                                                                                            Hol W,
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/note= "wild-type TCT(Ser) mutated to AAG(Lys)"
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                                                              English.
                                                                                                                                                                                                                                                                                                         Rappuoli
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                                                                                                                                             heat labile
o cholerae an
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                                                                                                                                             le toxin
and
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seq_documentation_block:
ID AAQ51318 standard;
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US-09-528-682-1 x
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Quality:
Ratio:
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                                                                                              misc_difference
                                                                                                                                         Escherichia
                                                                                                                                                              protomer A; site-directed mutagenesis;
ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                             enterotoxigenic bacteria; vaccine; immunogenic
                                                                                                                                                                                                                           Encodes Lys-97 E.coli heat labile toxin subunit
                                                                                                                                                                                                                                                     08-DEC-1993
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                                         WO9313202-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyValIleA 136
                                                                                                                                                                                                                                                                                                                                                                                   GTTGTGGA 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCATATTCTCAGATATATGGATGGTATCGTGTTAATTTTGGTGTGATTG
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1.000
100.000
                                                                                             Location/Qualifiers 277..279
                                                                 /note= "wild-type GTT(Val) mutated
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                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                              DNA;
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                 reduced
                                                                                                                                                                                 toxicity;
                                                                                                                                                                                                 detoxified LT-A;
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                                                                  AAG(Lys)"
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08-JUL-1993

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seq_documentation_block:
ID    AAQ51319 standard; DI
    XX
AC    AAQ51319;
XX
DT    08-DEC-1993 (first.)
                                                                                                  seq_name:
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US-09-528-682-1 x AAQ51318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51318 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino primer sequence used to introduce the preferred mutation. (Amino primer sequence used to introduce the preferred mutation.
                                                                                                                                                                                                                                                  445
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                                                                                                                                                           186
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                                                                                                                                                                                        OASPHISGINALATrPARGGIUGIUPTOTRPILEHISHISAlaPROGING
                                                                                                                                                                                                                                             eProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyValIleA 136
                                                                                                                                                                                                                                                                                                                                                                                                                        GTATACAGCCCTCACCCATATGAACAGGAGGTTTCTGCGTTAGGTGGAAT
                                                                                                                                GTTGTGGA
                                                                                                                                                          lyCysGly 188
                                                                                                                                                                                                                                                                                                                                                                 ACCATATTCTCAGATATATGGATGGTATCGTGTTAATTTTGGTGTGATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1993-227320/28.
                                                                                                  /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:AAQ51319
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Ratio:
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 (first entry)
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alignment_block:
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                                                                                                                                                                                                                                                                       Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic of useful as enterotoxin |
                                                                                                                                                                                                                                                                                                                                                                                                                                               The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to
                                                                                                                                                                                                                                                                                                                                                                             immunogenic, detoxified LT-A proteins and their use in vaccines protect against enterotoxigenic E.coli. Sequence AAO51319 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amir acid numbering is based on the cholera toxin A subunit sequence.)
                                                                 136
                                                                                            345
                                                                                                                       119
              153
                                        395
                                                                                                                                                 295 GTATACAGCCCTCACCCATATGAACAGGAGGTTTCTGCGTTAGGTGGAAT
                                                                                                                                                                            103
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 2 and Page 46; 60pp; English.
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P-PSDB; AAR44018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domenighini M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIOC-) BIOCINE
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ADP-ribosyltransferase activity; ss.
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                                                      spGluArgLeuHisArgAsnArgGluTyrArgAspArgTyrTyrArgAsn
                                                                                                         eProTyrSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyValIleA 136
                                                                                                                                                               ValTyrSerProHisProTyrGluGlnGluValSerAlaLeuGlyGlyIl
LeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProPr
                                                                                            ACCATATTCTCAGATATATGGATGGTATCGTGTTAATTTTGGTGTGATTG
                                        ATGAACGATTACATCGTAACAGGGAATATAGAGACCGGTATTACAGAAAT
                                                                                                                                                                                                                                                                                                  Quality:
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                                                                                                                                                                                                                                                                                                                                                       711 BP;
                                                                                                                                                                                                                                 x AAQ51319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detoxified mutant cholera toxin and heat labile vaccines against infection by Vibrio cholerae ar producing Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                       235 A;
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Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                       G; 197
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sis; reduced
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toxicity;
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               169
                                                                                                                                                                                                                                                                                                                                                                                  sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccines
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CTGAATATAGCTCCGGCAGAGGATGGTTACAGATTAGCAGGTTTCCCACC

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seq_documentation_block:
ID AAQ42768 standard; DN
XX AAQ42768;
XX O8-DEC-1993 (first e
XX enterotoxigenic bacte
KW protomer A; site-dire
KW protomer A; site-dire
KW ADP-ribosyltransferas
OS Escherichia coli.
XX Key Locat
FT mat_peptide 1..7(
FT /*tag
XX W09313202-A.
XX Immunogenic detoxifit
PF Juseful as vaccines
PF enterotoxin producing
XX Disclosure; Fig 2; 60
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                                           alignment_block:
US-09-528-682-1 x AAQ42768
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Align seg 1/1
                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                     This sequence encodes the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans. The sequence was published by Yamamoto et al, J.Bifect humans, 259, 5037-5044.

Mutations at selected positions within this sequence have been found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to

    useful as vaccines against intection
enterotoxin producing Escherichia coli

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protomer A; site-directed
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                                                                                                                                                                                                                                                                                                                                     protect against enterotoxigenic E.coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP-ribosyltransferase
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DB; AAR38728.
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                                                                                                                                                                              Quality:
                                                                                                                                                      Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detoxified mutant cholera toxin and heat labile toxin vaccines against infection by Vibrio cholerae and
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from:
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mutagenesis; reduced toxicity;
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tivity; ss.
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seq_documentation_block:
ID AAV81595 standard;
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                                                                                                                                                                                                                                                                                                                                                                               A subunit; heat labile toxin; ADP-ribosylation; mutant; detoxification; parenteral adjuvant; antigen; antigen; immunisation; humoral response; cell-mediated immune response; virus; bacterium; parasite; fungus; tumour; allergen; pathogen; AIDS; autoimmune disease; cancer; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136
                                                                                                             Detoxified mutants of bacterial ADP-ribosylating toxins as parenteral adjuvants - useful to enhance humoral and cell-mediated immune responses in vertebrates when administered with selected
                                                                                                                                                                                                                                                                                                                                                                      systemic lupus erythematosus; Alzheimer's
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                                                                              Disclosure;
                                                                                                  antigen e.g. in disease treatment
                                                                                                                                                           WPI; 1999-070064/06.
P-PSDB; AAW67772.
                                                                                                                                                                                              Barchfeld
                                                                                                                                                                                                                                           18-MAR-1998;
21-MAR-1997;
                                                                                                                                                                                                                                                                            19-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
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97US-0041227
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This sequence corresponds to the coding region for the A subunit of the E. coli heat labile toxin, an example of a bacterial ADP-ribosylating toxin. A mutant detoxified form of this protein is used in a parenteral adjuvant composition, which comprises the detoxified protein, at least one selected antigen and optionally a pharmaceutically acceptable (optionally topical) vehicle. The adjuvant composition can be

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seq_documentation_block:
ID AAQ51321 standard; DN
XX
AC AAQ51321;
XY
DT 08-DEC-1993 (first e
XX
Encodes Lys-104 E.col
XX
KW enterotoxigenic bacte
KW protomer A; site-dire
KW ADP-ribosyltransferas
XX
OS Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              administered parenterally in conjunction with at least one antigen in methods to immunise vertebrate subjects. The adjuvant has the ability to enhance the humoral and cell-mediated immune responses elicited by the antigen (e.g. by making the antigen more strongly immunogenic or necessitating fewer/lower antigen doses). It can be administered
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                                                                     ADP-ribosyltransferase activity; ss
                                                                                            enterotoxigenic bacteria; vaccine; immunogenic detoxified protomer A; site-directed mutagenesis; reduced toxicity;
                                                                                                                                                                                           Encodes Lys-104 E.coli heat labile toxin subunit A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 711 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOC-) BIOCINE SCLAVO SPA.
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-7
                                       CCAAGCTTGGAGAGAACCCTGGATTCATCATGCACCACAAGGTTGTG
                                                                                              IleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProProAspHi
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                                                 Align
                                                                        US-09-528-682-1 x AAQ51322
                                                                                                           Percent Similarity:
                                                                                                                                                                                                     The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51322 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino acid numbering is based on the cholera toxin A subunit sequence).
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1993-227320/28.
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XX WO9313202-A.
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XX WPI; 1993-227320/28.
PR P-PSDB; AAR44022.
XX WPI; 1993-227320/28.
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   The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42788) was subjected toxic-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51323 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino acid numbering is based on the cholera toxin A subunit sequence).
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                                                                                                                                                                                                                                                                                                                                                                                            Immunogenic detoxified mutant cholera toxin and heat labile toxin - useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAAGCTTGGAGAGAACCCCTGGATTCATCATGCACCACAAGGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATAGCTCCGGCAGAGGATGGTTACAGATTAGCAGGTTTCCCCACCGGATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyValIleAspGluA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1993-227320/28
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                                                                                                                                                                                                                                                                                                                                        3; Fig 2 and Page 46; 60pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92WO-EP03016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 298..300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rappuoli
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alignment_block:
US-09-528-682-1 x AAQ51323
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seq_documentation_block:
ID AAQ51324 standard;
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                        30-DEC-1992;
                                                                                                                                                misc_difference
                                                                                                                                                                                                       enterotoxigenic bacteria; vaccine; immunogenic detoxified LT-A;
protomer A; site-directed mutagenesis; reduced toxicity;
                                                                                                                                                                                                                                                     08-DEC-1993
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WPI; 1993-227320/28
                  Domenighini M,
                                                       31-DEC-1991;
                                                                                           08-JUL-1993
                                                                                                            W09313202-A
                                                                                                                                                                            Escherichia
                                                                                                                                                                                              ADP-ribosyltransferase
                                                                                                                                                                                                                                   Encodes Ser-106 E.coli heat labile toxin subunit A.
                                    (BIOC-) BIOCINE
                                                                                                                                                                                                                                                                                                                                                                         rSerGlnIleTyrGlyTrpTyrArgValAsnPheGlyValIleAspGluA 138
                                                                                                                                                                                                                                                                                                                                                                                                            GA 552
                                                                                                                                                                                                                                                                                                                                                        ly 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCCCTCACCCATATGAACAGGAGGTTTCTGCGTTAGGTGGAATACCATA
                                                                                                                                                                                              A; site-directed mutagenesis;
syltransferase activity; ss.
                                                                                                                                                                            coli.
                                                                                                                                                                                                                                                    (first entry)
                                                       91IT-0MI3513
                                                                        92WO-EP03016
                                                                                                                                                Location/Qualifiers 304..306
                  Hol W,
                                   SCLAVO SPA
                                                                                                                              /*tag=
/note=
                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                              "wild-type CCT(Pro) mutated
                                                                                                                                                                                                                                                                                          711
                   Pizza
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Identity:
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seq_documentation_block:
ID AAQ51320 standard; DN
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AC AAQ51320;
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AC AAQ51320;
XX
Encodes Glu-107 E.col
XX
Encodes Glu
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US-09-528-682-1 x AAQ51324
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                       enterotoxigenic bacteria; vaccine; immunogenic detoxified LT-A;
protomer A; site-directed mutagenesis; reduced toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     507
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                                                                                                                                                                                                                          ADP-ribosyltransferase
                                                                                                                                                                                                                                                                                                                                                      Encodes Glu-107 E.coli heat labile toxin subunit A.
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                                                                 Location/Qualifiers 307..309
      /note=
                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
      "wild-type CAC(His) mutated to GAG(Glu)"
                                                                                                                                                                                                                             activity;
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Gaps:
Percent Identity:
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seq_documentation_block:
    ID     AAQ51325 standard;     DN
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    AC     AAQ51325;
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US-09-528-682-1 x AAQ51320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 81.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                    510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOC-) BIOCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-DEC-1991;
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                                                                                                                                eTyrGlyTrpTyrArgValAsnPheGlyValIleAspGluArgLeuHisA 141
                                                                                                                                                                                                                     AlaGluAspGlyTyrArgLeuAlaGlyPheProProAspH1sGlnAlaTr 174
                                                                                                                                                                                                                                                                                      rgAsnArgGluTyrArgAspArgTyrTyrArgAsnLeuAsnIleAlaPro
                                                                                                                                                                                                                                                                                                                                                                                                                            ProTyrGluGlnGluValSerAlaLeuGlyGlyIleProTyrSerGlnI1 124
                                                                                                                                                                                                                                                                    GTAACAGGGAATATAGAGACCGGTATTACAGAAATCTGAATATAGCTCCG
                                                                                                                                                                                                                                                                                                                                       ATATGGATGGTATCGTGTTAATTTTGGTGTGATTGATGAACGATTACATC
                                                                                                                                                                                                                                                                                                                                                                                                         CCATATGAACAGGAGGTTTCTGCGTTAGGTGGAATACCATATTCTCAGAT 359
                                                                                                                                                                                                 GCAGAGGATGGTTACAGATTAGCAGGTTTCCCACCGGATCACCAAGCTTG
                                                 standard; DNA; 711 BP
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                                                                                                                                                                                                                                                                             The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51325 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino acid numbering is based on the cholera toxin A subunit sequence).
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  165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Fig 2 and Page 46; 60pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAR44024.
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                                                                                                                                                                                           nPheGlyValIleAspGluArgLeuHisArgAsnArgGluTyrArgAspA 148
AlaGlyPheProProAspHisGlnAlaTrpArgGluGluProTrpIleHi 181
                                                                                                                                                                    TTTTGGTGTGATTGATGAACGATTACATCGTAACAGGGAATATAGAGACC
                                                    GGTATTACAGAAATCTGAATATAGCTCCGGCAGAGGATGGTTACAGATTA
                                                                                       rgTyrTyrArgAsnLeuAsnIleAlaProAlaGluAspGlyTyrArgLeu
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ID AAQ51326 standard;
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Percent Similarity:
                                                                                                                                                                    The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51326 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino acid numbering is based on the cholera toxin A subunit sequence).
                                                                                                                                                                                                                                                                                                                                           Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                               Sequence
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/note= "wild-type TCT(Ser)
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seq_documentation_block:
ID AAT03448 standard;
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US-09-528-682-1 x
                                 Percent Similarity:
                                                                                                                           The present sequence is that of the LTf fragment which encodes part of the thermolabile enterotoxin subunit-A sequence and all of the subunit-B sequence of Shigella flexneri. The DNA fragment is useful as a probe for specific detection of toxigenic enterobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       531
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                                                                                                                                                                                        Claim 1; Columns 3-4; 5pp; Russian.
                                                                                                                                                                                                                         LTf DNA fragment for recognition of thermo:labile enterobacterium enterotoxin gene - can be used as a probe for recognition of
                                                                                                                                                                                                                                                             WPI; 1995-343066/44.
                                                                                                                                                                                                                                                                                    Mazepa
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                                                                                                                                                                                                                                                                                                                                                                                                                             Shigella flexneri.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shigella flexneri thermolabile enterotoxin gene
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                                                                                                      Sequence 777
                                                                                                                                                                                                                                                                                                           (NIZH=) NIZHEGOROD EPIDEMIOLOGY MICROBIOLOG INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     fragment; enterobacteria; ss.
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seq_documentation_block:
ID AANJO099 standard; DN
AC AANJO099;
XX AC AANJO099;
XX AC AANJO099;
XX CENTEROLOXOId; Immunog
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                                                                   The inventors claim pEBK620 and bacterial strains obtd. by transforming E.coli K12 5K with it. pEBK620 is prod. by cleaving pEFK295 with HiddII, cleaving pKS100 with Hidd III and treating pEFK295 with alkaline phosphatase, ligating, transforming E.coli K12 F 165 delta (gal)-trp, selecting ampicillin-resistant transformants, and isolating a recombinant plasmid contg. 111, 196, 196 and 780 bp fragments of pEFK295. The fragment in AN30099 begins with the
                                                                                                                                                                                                                                                                                                            Plasmid(s) coding for entero-toxoid strains transformed with such plasm:
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seq_documentation_block:
ID AAF74431 standard;
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US-09-528-682-1 x
       CC Vibrio cholerae nucleic acid by: (a) performing a polymerase chain cc reaction (PCR), by combining a medium containing toxigenic V. cholerae nucleic acid with an oligonuclectide primer (I) which will bind to a containing toxigenic V. cholerae containing toxigenic V. cholerae cc section of V. cholerae nucleic acid, in an environment suitable for cc carrying out PCR; (b) combining the medium with a second primer which cc will bind downstream to the first primer to a section of the complementary strand of the V. cholerae nucleic acid; and (c) amplifying corresponding sections of V. cholerae nucleic acid present in the medium. CC the method is useful for detecting toxigenic V. cholerae organisms or cc toxigenic V. cholerae nucleic acid, e.g., ctxA gene, in an environmental cc water sample e.g., tap water sample, river water sample, lake water cc sample or a sewage sample. The method is useful in PCR assays for cc detecting a microorganism or nucleic acid of the microorganism in a cc sample. (I) and amplification products are useful for detecting toxigenic CC V. cholerae nucleic acid in a sample. The PCR method involving (I) is creiton from the V cholerae cran cannot seem to genence represents a cc region from the V cholerae cran cran suches to constitute for detecting toxigenic confidence in water samples. The present sequence represents a cc region from the V cholerae cran cran suches to constitute for detecting toxigenic confidence confidence confidence cran cannot cran cannot cran cannot constitute for detecting toxigenic confidence confidence confidence cannot cannot constitute for detecting toxigenic confidence confidence confidence cannot can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Fig 7; 44pp; English.
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         The present invention describes a method for amplifying (A1) toxigenic Vibrio cholerae nucleic acid by: (A) performing a polymerase chain creaction (PCR), by combining a medium containing toxigenic V. cholerae nucleic acid with an oligonucleotide primer (I) which will bind to a containing toxigenic V. cholerae nucleic acid, in an environment suitable for carrying out PCR; (b) combining the medium with a second primer which will bind downstream to the first primer to a section of the complementary strand of the V. cholerae nucleic acid; and (c) amplifying corresponding sections of V. cholerae nucleic acid present in the medium. The method is useful for detecting toxigenic V. cholerae organisms or toxigenic V. cholerae nucleic acid, e.g., ctxA gene, in an environmental water sample or a sewage sample. The method is useful in PCR assays for detecting a microorganism or nucleic acid of the microorganism in a detecting a microorganism or nucleic acid of the microorganism in a
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amplification products are useful
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-528-682-1 x AAF74430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V. cholerae nucleic acid in a sample. The PCR method involving (I) rapid, economical, specific and sensitive for detecting toxigenic V. cholerae in water samples. The present sequence represents a region from the V. cholerae ctxA gene, which is used in an example the present invention.
The wild-type sequence coding for the A subunit of the cholera toxin (CT-A) (Mekalanos et al., Nature 306, 551 (1983) - see AAQ46318) was subjected to site-directed mutagenesis. Certain mutations were
                                                                    Immunogenic detoxified mutant cholera toxin and heat labile toxin - useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                               Claim 3; Fig 2 and Page 48; 60pp; English
                                                                                                                                                                                                                              30-DEC-1992;
                                                                                                                                                                                                                                                                                                                            misc_difference
                                                                                                                                                                                                                                                                                                                                                              Vibrio
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                                                                                                                        P-PSDB; AAR44027
                                                                                                                                                        Domenighini M,
                                                                                                                                                                               (BIOC-) BIOCINE SCLAVO SPA
                                                                                                                                                                                                         31-DEC-1991;
                                                                                                                                                                                                                                                      08-JUL-1993
                                                                                                                                                                                                                                                                             WO9313202-A
                                                                                                                                                                                                                                                                                                                                                                                                  protomer A;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Encodes Lys-63 cholera toxin
                                                                                                                                   WPI; 1993-227320/28.
                                                                                                                                                                                                                                                                                                                                                                                    ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic
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                                                                                                                                                                                                                                                                                                                                                              cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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                                                                                                                                                                                                                                                                                                                                                                                                site-directed mutagenesis;
                                                                                                                                                                                                                                                                                                                                                                                                           detoxified CT-A; cholera vaccine; adenylate cyclase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                          Ho1
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                                                                                                                                                                                                                                                                                                     /note= "wild-type TCA(Ser) mutated to AAG(Lys)"
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                                                                                                                                                                                                                                                                                                                 /*tag=
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Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564
                                                                                                                                                                                                                                                                                                                                                                                                  reduced toxicity;
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alignment_block:
US-09-528-682-1 x AAQ51328
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ID AAQ51329 standard;
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic detoxified protomer A; site-direct ADP-ribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found to reduce toxicity (see AAQ51327-Q51334). The invention relates to inmunogenic, detoxified CT-A proteins and their use in vaccines to protect against Vibrio cholerae. Sequence AAQ51328 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation.
The wild-type sequence coding for the A subunit of the cholera toxin (CT-A) (Mekalanos et al., Nature 306, 551 (1983) - see AAQ46 was subjected to site-directed mutagenesis. Certain mutations were
                                                                             Immunogenic detoxified mutant cholera toxin and heat labile toxin - useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                    Claim 3; Fig
                                                                                                                                                                                                                                                                                08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Encodes Lys-97 cholera toxin subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 723 BP;
                                                                                                                                   P-PSDB;
                                                                                                                                                                        Domenighini M,
                                                                                                                                                                                                                             31-DEC-1991;
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                                                                                                                                                                                                                                                                                                                                                              misc_difference
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                                                                                                                                                                                                   (BIOC-) BIOCINE
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                                                                                                                                              1993-227320/28.
                                                                                                                                   AAR44028
                                                                                                                                                                                                                                                                                                                                                                                                                              detoxified CT-A; cholera vaccine; adenylate
    site-directed mutagenesis; reduced toxicity;
    transferase activity; ss.
                                                   2 and Page 48; 60pp; English.
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                                                                                                                                                                                                                                                      92WO-EP03016
                                                                                                                                                                        Hol W,
                                                                                                                                                                                                   SCLAVO SPA
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 289..291
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                                                                                                                                                                                                                                                                                                                                 /note= "wild-type GTT(Val) mutated
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Gaps:
Identity:
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                                                                                                                                                                       Rappuoli
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             AAQ46318)
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alignment_block:
US-09-528-682-1 x AAQ51329
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The wild-type sequence coding for the A subunit of the cholera toxin (CT-A) (Mekalanos et al., Nature 306, 551 (1983) - see A was subjected to site-directed mutagenesis. Certain mutations
                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic detoxified CT-A; cholera vaccine; a protomer A; site-directed mutagenesis; reduced ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135
                                                 Claim 3;
                                                                        Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                       WPI;
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                                                                                                                                                                                                                                                                                                                                                                             Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Encodes Ser-106 cholera toxin subunit
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                                                                                                                            P-PSDB;
                                                                                                                                                             Domenighini M,
                                                                                                                                                                                                                                                                                       W09313202-A.
                                                                                                                                                                                     (BIOC-) BIOCINE SCLAVO SPA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGAGGAACTCAGACGGGATTTGTTAGG
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                                                 Fig 2 and
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                                                                                                                                                                                                               91IT-0MI3513
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                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 316..318
                                                                                                                                                                                                                                                                                                             /note= "wild-type CCT(Pro)
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                                                 Page 48;
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                                                 English.
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100.000
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d toxicity;
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              AAQ46318)
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seq_documentation_block:
ID AAQ51331 standard; DN
XX AC AAQ51331;
XX DT 08-DEC-1993 (first 6
XX Encodes Asn-107 chole
XX Immunogenic detoxifie
KW protomer A; site-dire
KW protomer A; site-dire
XX Immunogenic cholerae.
XX Kw protomer A; site-dire
XX Immunogenic detoxifie
KW protomer A; site-dire
XX Immunogenic cholerae.
XX Vibrio cholerae.
XX PPN W09313202-A.
XX N09313202-A.
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XX PPN W09313202-A.
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US-09-528-682-1 x AAQ51330
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                          Immunogenic detoxified mutant cholera toxin and heat labil - useful as vaccines against infection by Vibrio cholerae enterotoxin producing Escherichia coli
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  The wild-type sequence coding for the A subunit of the cholera toxin (CT-A) (Mekalanos et al., Nature 306, 551 (1983) - see A was subjected to site-directed mutagenesis. Certain mutations
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                                                                                                                  3; Fig 2 and Page 48; 60pp; English
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                                                                                                                                                                                                                                                                                                                                                                                 HOl W,
                                                                                                                                                                                                                                                                                                                                                                                                                                      SCLAVO
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                                             Claim 3; Fig 2 and Page 48; 60pp; English.
                                                                  Immunogenic detoxified mutant cholera toxin and l useful as vaccines against infection by Vibrio enterotoxin producing Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                            protomer A; site-directed mutagenesis;
ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                                                                                                                                                         Immunogenic detoxified CT-A; cholera vaccine; adenylate cyclase;
protomer A; site-directed mutagenesis; reduced toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                        Encodes Ser-110 cholera toxin subunit
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The wild-type sequence coding for the A subunit of the cholera toxin (CT-A) (Mekalanos et al., Nature 306, 551 (1983) - see AAQ46318) was subjected to site-directed mutagenesis. Certain mutations were

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   ID AAQ51333 standard;
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US-09-528-682-1 x AAQ51332
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                                                                        Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
The wild-type sequence coding for the A subunit of the cholera toxin (CT-A) (Mekalanos et al., Nature 306, 551 (1983) - see A was subjected to site-directed mutagenesis. Certain mutations
                                                Claim 3; Fig 2 and Page 48; 60pp;
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                                                                                                                                                                                                                                                                                                                                                                            Vibrio
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                                                                                                                                       WPI; 1993-227320/28.
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                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 334..336
                                                                                                                                                                                                                                                                                                             /note= "wild-type GAA(Glu) mutated
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US-09-528-682-1 x AAQ51333
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Ratio: 1.000
Percent Similarity: 100.000
The wild-type sequence coding for the A subunit of the cholera toxin (CT-A) (Mekalanos et al., Nature 306, 551 (1983) - see A was subjected to site-directed mutagenesis. Certain mutations
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                                                                          Immunogenic detoxified mutant cholera toxin and heat labile t - useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
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                                                    Claim
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                                                                                                                                                                   Rappuoli
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0
100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                         adenylate cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                               toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134
                                                                                                      toxin
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8288888888888
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    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-528-682-1 x AAQ51334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found to reduce toxicity (see AAQ51327-Q51334). The invention relates to immunogenic, detoxified CT-A proteins and their use in vaccines to protect against vibrio cholerae. Sequence AAQ51334 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation.
This sequence encodes the A subunit of the cholera toxin (CT-A) of Vibrio cholerae. The sequence was published by Mekalanos et Nature 306, 551 (1983). Mutations at selected positions within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135
                                                  Disclosure; Fig 2; 60pp; English.

    useful as vaccines against infection
enterotoxin producing Escherichia coli

                                                                                                                                                                 Domenighini M,
                                                                                                                                                                                                                  31-DEC-1991;
                                                                                                                                                                                                                                          30-DEC-1992;
                                                                                                                                                                                                                                                                    08-JUL-1993
                                                                                                                                                                                                                                                                                                                                           mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cholera toxin subunit A coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ46318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ46318 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                     Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                              P-PSDB;
                                                                                                                                                                                         (BIOC-) BIOCINE
                                                                                                                                                                                                                                                                                           W09313202-A
                                                                                                                                                                                                                                                                                                                                                                                                       ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic protomer A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aArgGlyThrGlnThrGlyPheValArg 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAl 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGTACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGAGGAACTCAGACGGGATTTGTTAGG
                                                                                                                            1993-227320/28.
DB; AAR38729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:AAQ46318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  723 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: AAQ51334
                                                                                                                                                                                                                                                                                                                                                                                                                   site-directed mutagenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                              detoxified CT-A; cholera vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                  91IT-0MI3513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.00
1.000
100.000
                                                                                                                                                                                                                                        92WO-EP03016
                                                                                                                                                                                         SCLAVO
                                                                                                                                                                 Hol W,
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229
                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; 124 C;
                                                                                                                                                                                                                                                                                                        a
"CT-A"
                                                                                                                                                                                         SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               723
                                                                                                                                                                 Pizza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent
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                                                                                                                                                                 ĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identity:
                                                                                                                                                               Rappuoli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>:</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                    reduced
                                                                                                                                                                 æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 26
: 0
: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                            adenylate cyclase;
                                                                                                                                                                                                                                                                                                                                                                                                                    toxicity;
              al.,
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SSSSS
seq_documentation_block:
ID AAV81596 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-528-682-1 x AAQ46318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                  A subunit; heat labile toxin; ADP-ribosylation; mutant; detox parenteral adjuvant; antigen; antigen; immunisation; humoral; cell-mediated immune response; virus; bacterium; parasite; fur tumour; allergen; pathogen; AIDS; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135
                                                                                     Disclosure; Fig 1A-B; 51pp; English.
                                                                                                                                                                                                                                                                                        01-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                        systemic lupus erythematosus; Alzheimer's disease; diagnosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                        Cholera toxin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV81596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence have been found to reduce toxicity invention relates to immunogenic, detoxified use in vaccines to protect against cholera.
                                                                                                            antigen
                                                                                                                                                                  WPI; 1999-070064/06.
                                                                                                                                                                                       Barchfeld
                                                                                                                                                                                                                                  18-MAR-1998;
21-MAR-1997;
                                                                                                                                                                                                                                                                                                                                   Vibrio cholerae.
                                                                                                                                  parenteral adjuvants - useful to enhance
                                                                                                                                            Detoxified
                                                                                                                                                                                                                                                                  19-MAR-1998;
                                                                                                                                                                                                                                                                                                              WO9842375-A1
                                                                                                                     immune responses in vertebrates when
                                                                                                                                                                                                            (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aArgGlyThrGlnThrGlyPheValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGTACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGAGGAACTCAGACGGGATTTGTTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS5/gcgdata/geneseg/geneseqn-embl/Na1999.DAT:AAV81596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                          e.g. in disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                      G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: AAQ46318
                                                                                                                                 mutants of bacterial ADP-ribosylating adjuvants - useful to enhance humoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                       Del Giudice
                                                                                                                                                                                                                                 98US-0044696
97US-0041227
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1.000
100.000
                                                                                                                                                                                                                                                                   98WO-US05454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Α;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125
                                                                                                            treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          723 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from:
                                                                                                                                                                                    ,
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent
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                                                                                                                                                                                      Rappuoli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Gaps:
Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detoxified
                                                                                                                      administered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (see AAQ51327-Q51334). The CT-A proteins and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
0
. 000
                                                                                                                                                                                                                                                                                                                                                                                                   mutant; detoxification;
                                                                                                                                 and
                                                                                                                                            toxins
                                                                                                                      with selected
                                                                                                                                 ins as
cell-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134
                                                                                                                                                                                                                                                                                                                                                                           fungus
                                                                                                                                                                                                                                                                                                                                                                                        response;
                                                                                                                                                                                                                                                                                                                                                                    antibody;
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This sequence corresponds to the coding region for the A subunit of the cholera toxin, an example of a bacterial ADP-ribosylating toxin. A mutant detoxified form of this protein is used in a parenteral adjuvant composition, which comprises the detoxified protein, at least one selected antigen and optionally a pharmaceutically acceptable (optionally topical) vehicle. The adjuvant composition can be administered

parenterally

in

conjunction

with

least one

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alignment_block:
US-09-528-682-1 x AAV81596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cc immunise vertebrate subjects. The adjuvant has the ability to enhance ct the humoral and cell-mediated immune responses elicited by the antigen cc (e.g. by making the antigen more strongly immunogenic or necessitating cc fewer/lower antigen doses). It can be administered prior/subsequent to the antigen, and is preferably administered within a short space of time ct to the same site; it can also be administered in isolation from antigens cas a boost following systemic or nucosal antigen administration. Most corpeterably, the adjuvant is co-administered with the antigen in the compositions and a pharmaceutically acceptable carrier. The antigen may cc be derived from viruses, bacteria, parasites and fungi or may be tumour cantigens, self-antigens and allergens. The compositions are therefore cc useful in the treatment and prevention of e.g. viral diseases, allergic manifestations, diseases caused by pathogens (e.g. bacteria or cc parasites), Alzheimer's disease (e.g. Systemic Lupus cc parasites), Alzheimer's disease and cancers. The adjuvant can also be used to prepare antibodies against selected antigen(s), useful cc e.g. for diagnostic purposes or for antigen purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AAV81596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135
                (BOYC-) BOYCE THOMPSON INST PLANT RES (MASO/) MASON H S. (ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                            Plant-optimized V. cholerae toxin A subunit coding sequence
                                                                                                                                                                                                                                                                                                                                                                          Heat-labile toxin; CT-A; CT-B; mutant; transgenic plant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 723 BP; 227 A; 125 C; 163 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 aArgGlyThrGlnThrGlyPheValArg 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGAGGAACTCAGACGGGATTTGTTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAA51157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                          Location/Qualifiers
1..777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.00
1.000
                                                                                                                                                                                                                          /product= cholera_toxin_subunit_A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 other;
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alignment_block:
US-09-528-682-1 x AAA51157
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA51158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AAA51157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This plant-codon optimized cDNA encodes a synthetic Vibrio cholerae cholera toxin (CT) A subunit (CT-A). The sequence has no cryptic signal sequence and no CG (potential methylation sites) sequences. Novel polynucleotides encode a mutant Escherichia coli heat-labile toxin (LT) subunit A (LT-A) polypeptide or a mutant V. cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CTB subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the prophylactic or therapeutic treatment against E. coli or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189
                29-JUN-2000
                                                 WO200037609-A2
                                                                                                                                                                     Synthetic
                                                                                                                                                                                     Vibrio cholerae
                                                                                                                                                                                                                     adjuvant; anti-bacterial;
                                                                                                                                                                                                                                       Heat-labile toxin; CT-A; CT-B; mutant; transgenic plant; vaccine; oral;
                                                                                                                                                                                                                                                                       Plant-optimized mutant V. cholerae toxin A subunit K63 coding sequence.
                                                                                                                                                                                                                                                                                                           26-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                           AAA51158 standard; cDNA; 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 777 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V. cholerae. The mutant polypeptides are also useful as adjuvants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 4A; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions of plant cells, useful in immunogenic compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY96653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-442653/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 aArgGlyThrGlnThrGlyPheValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGGGGAACTCAAACTGGATTTGTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
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                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.000
                                                                                                                   Location/Qualifiers
1..777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209
                                                                              /product= mutant_cholera_toxin_subunit_A
                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.00
1.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; 174 C; 191 G; 203 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                       S63K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 26
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                       SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54
                                                                                                                                                                                                                                                                                                                                                                                                                                                              216
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45
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alignment_block:
US-09-528-682-1 x AAA51158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AAA51158
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Percent Similarity:
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     Key
                                                                                                                              Heat-labile toxin; CT-A; CT-B;
adjuvant; anti-bacterial; A72R;
                                                                                                                                                                                                    Plant-optimized mutant V. cholerae toxin A subunit R72 coding sequence
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                                                                              Vibrio cholerae
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                                                                                                                                                                                                    Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                        US-09-528-682-1 x AAN30169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The inventors claim a sequence contg. at least one fragment coding for all or part of sub-units A and B of cholera toxin. The entire sequence and two fragments (FI and F2) are listed in the specification. Also new are recombinant DNA molecules contg. these sequences (spec. pRIT 18014 contg. the whole sequence; pRIT 18014 contg. the whole sequence; pRIT 18016 contg. F1 and pRIT 10810 contg. F2) and transformed host cells (spec. coli ATCC 39052 contg. The whole sequence, ATCC 39053 contg. F1 and ATCC 39051 contg. F2).
                                                                                                      139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence coding for cholera toxin sub units transforming host cells, useful in vaccine produ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence of pRIT 18014 encoding sub-unit A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAN30169 standard; DNA; 1148
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aArgGlyThrGlnThrGlyPheValArg
                                                                                                 cholera; subunit A;
                                                                                                                                                                                                                                                                                                                                                           Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 382
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                                                                                                                                                                                                          AAN30169
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/label= F1
/note= "claimed:
774..1148
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/label=
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1..777
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Percent Identity:
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                                                                                                      188
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189

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seq_documentation_block:
ID AAI67270 standard; DN
AC AAI67270;
AC AAI6
                       alignment_scores:
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                                                                                                                                                                                                                                                                                                                    enterotoxin which has been mutated to provide A subunit. A composition of matter comprising the chimeric molecule in a pharmaceutically acceptable carrier is useful for obtaining enhanced immune response of an organism to an antigen by administering it to the antigen. The chimeric molecule is useful to provide specific immune reasonees to
                                                                                                                                                                                                                                                     is useful to provide specific immune response to a particular enterotoxin, as adjuvants for use with unrelated vaccines, and to customize adjuvants to direct production of cell-mediated or humoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides a chimeric molecule that comprises a first subunit which is mutated A subunit of first enterotoxin and a second non-mutated subunit from a second enterotoxin which is different from the natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric molecule useful as adjuvant for cell-mediated/humoral immunity comprises first mutated A subunit of first enterotoxin and second non-mutated subunit from second enterotoxin different from natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 4; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAR-2000; 2000US-190058P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI67270 standard; DNA; 2056 BP
                                                                                                                                                                                               immune responses. It is also useful as mucosal adjuvant or humoral immunity. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAI67270
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG65991, AAG65992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kiyono H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-US08582
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                                                                                                                                                                          A and B subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOUND
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/product= "Cholera toxin
/note= "AAG65991"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   551..1327
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1699..2056
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/note= "AAG65992"
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                                                                                                                 327 C;
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                                                                                                                 G; 647
Length:
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                                                                                                                 Τ,
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                                                                                                                                                                                                     the DNA sequence
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seq_name:
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                                                                                                        therapeutically treating an animal with a therapeutic agent encoded by polynucleotide coding sequence, by transfecting the animal with a bacterial bleb containing a eukaryotic expression cassette including the polynucleotide coding sequence. The method can be used for introducing endogenous or foreign genes into animal cells using bacterial blebs as vectors. The method allows for the delivery of eukaryotic expression
                                                                                                                                                                                                                                                            The present invention also describes: (1) a bacterial bleb containing a eukaryotic expression cassette; (2) a transformed animal cell including a bacterial bleb, or a transfected product of the bacterial bleb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Introducing and expressing a gene in animal cells, useful for delivering a therapeutic agent to the cells, comprises infecting animal cells with bacterial blebs containing a eukaryotic expression cassette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    689 GAGTACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCATGC
containing the eukaryotic expression cassette can also animal cells cultured in vitro. The method can be used
                                 therapeutic agents, immunoregulatory agents, antisense RNAs, a catalytic RNAs in animal cells or tissues. The bacterial blebs
                                                      cassettes encoding the endogenous or foreign genes into animal cells or tissues, and is useful for expressing e.g. vaccine antigens, gene therapeutic agents, immunoregulatory agents, antisense RNAs, and
                                                                                                                                                                                                                                                                                                                    a gene in animal cells, comprising infecting animal cells with bacte blebs containing a eukaryotic expression cassette encoding the gene.
                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for introducing and expressing a qene in animal cells, comprising infecting animal cells with bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholera toxin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            739
                                                                                                                                                                                                                         (3) a method of delivering a eukaryotic expression cassette to an
animal cell, comprising mucosal transfection; and (4) a method of
                                                                                                                                                                                                                                                                                                                                                                                                Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Powell RJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABA92644;
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                                                                                                                                                                                                                                                                                                                                                                                              English.
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Percent Identity: 100.000
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                   be used
                                                                                                                                                                       including the
                 to treat
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gene

therapy

SSSSS

The present sequence represents the cholera toxin Al subunit sequence, which is used in an example from the present invention for the product of non-pyrogenic blebs containing a DNA vaccine.

the production

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seq_documentation_block:
ID AAQ12710 standard; DN
XX AAQ12710;
XX AAQ12710;
XX AAQ12710;
XX AAQ12710;
XX AAQ12710;
XX OB-OCT-1991 (first & XX Cholera toxin Al frag
XX Hybrid; fusion; memb)
KW infection; toxin; standard; exotoxin, a;
XX Hybrid; fusion; memb)
KW infection; toxin; standard; exotoxin, a;
XX Vibrio cholera.
XX Vibrio chole
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US-09-528-682-1 x ABA92644
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Quality: 26.00
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hybrid; fusion; membrane translocation; binding region; HIV; infection; toxin; steroid; hormone; monoclonal antibody; antigen; diphtheria; exotoxin; phenylketonuria; cholera; interleukin; IL-2; protease; epidermal growth factor; ricin; tetanus; hexosaminidase; Shiga-like toxin A; ligand; insulin; nuclease; ss.
                                                                                                                                              Hybrid molecules for targetting chemical entity to cell - membrane trans-locating and cell binding-regions and used treat HIV infection, genetic enzyme-deficiency disorders e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cholera toxin Al fragment.
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  Hybrid molecules are produced by covalently linking (1) a portion (A) of the binding domain of a cell-binding ligand,
                                                                                            Disclosure; F1g 5(1-2); 59pp; English.
                                                                                                                                                                                                                                                                      WPI; 1991-222845/30.
P-PSDB; AAR13117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGAGGAACTCAGACGGGATTTGTTAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90US-0538276.
89US-0456095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90WO-US07619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag-
/label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1619 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA; 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CT-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
6
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                                                                                                                                                       etc.
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:AAT91636
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US-09-528-682-1 x AAQ12710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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sequence), Illume
malease, etc.
                                                                                                                                                                                                                                               Cholera toxin A1; hybrid protein; cell delivery; cell binding ligand; translocation domain; dipht interleukin-2; leukaemia; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Specified examples are CT-A/DT-B'/IL-2, SLTA/DT-B'/IL-2, ricin A/DT-B'/IL-2, HIVP-BP/DT-B'/IL-2 and the phenylalanine hydroxylase-DT-B' or their biologically active mutants. (CT-A- cholera toxin, DT-B'= truncated diphtheria toxin, SLTA- Shiga-like toxin A; HIVP-BP- HIV protease binding protein. See also AAQ12710-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allowing binding of the mol. to an animal cell; (2) a portion (B) of a translocation domain of a protein able to translocate (C) across the cell cytoplamic membrane, and and (3) a portion (C) which is to be introduced into the cell. (A) is derived from a steroid or polypeptide hormone, a single-chain analogue of a monoclonal antibody able to bind an antigen expressed on the cell surface, or a polypeptide toxin.

(B) is derived from a toxin (e.g. diphtheria toxin or Pseudomonas
                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epidermal growth factor.
Suitable enzymes in (C) include cholera toxin (encoded by this sequence), ricin, tetanus toxin, hexosamininidase A, protease,
27-JUN-1991;
07-JUN-1984;
                                                                                                                                                                                                                                                                                                         Vibrio cholerae toxin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exotoxin A).
(A) may be derived from insulin, interleukins 2,
                                            07-JUN-1984;
                                                                         16-SEP-1997
                                                                                                    US5668255-A
                                                                                                                                                                                                                     Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                    27-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                    AAT91636;
                                                                                                                                                                                                                                                                                                                                                                                              AAT91636 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 TACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCATGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 780 BP; 243 A; 130 C; 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 TyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gGlyThrGlnThrGlyPheValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
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91US-0722484
84US-0618199
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1..777
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/transl_except= (pos:616..618,
                                                                                                                                                             /*tag=
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Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                 ВP
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0
                                                                                                                                                                                                                                                domain; diphtheria toxin ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          780
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                                                                                                                                 aa:Ala)
aa:Ala)
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XX DE XX DE XX DE XX
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                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence comprises the Vibrio cholerae gene that encodes CC cholera toxin (see AAW25785). DNA encoding an enzymatically active Al fragment of the cholera toxin was used to construct a cholera CC toxin Al-diphtheria toxin B'-interleukin-2 (CTA-DTB-IL2) gene that CC was expressed in E. coli. The hybrid protein can be isolated and CC used e.g. as an adjunct to treatment with DTB-IL2 hybrid, which CC targets the cell-killing ability of diphtheria toxin to cells CC bearing the IL2 receptor, such as certain leukaemic T cells. Prior application of the CTA-DTB-IL2 hybrid alleviates the CC prior application of the CTA-DTB-IL2 hybrid alleviates the CC problem of endogenous IL2 competing with DTB-IL2 hybrid for IL2 creceptors on T cells. Claimed hybrid proteins comprise a cc translocation domain and a cell binding domain from e.g. a hormone, CC growth factor or polypeptide toxin. The hybrid molecules can be CC used for the delivery of agents (e.g. therapeutic genes, toxins, CC detectable labels) into cells. The use of a translocation cc detectable labels) into cells. The use of a translocation cc mechanism ensures that the hybrid will be effective in relatively CC low doses, since a high proportion of the substance of interest CC will be taken into the targeted cells. The hybrid molecules can be CC manufactured as a single hybrid recombinant protein, permitting CC composition.
                                                                                                                                                                                                                                                                                                                                          Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                          US-09-528-682-1 x AAT91636
                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-APR-1985;
07-JUN-1985;
22-DEC-1989;
14-JUN-1990;
                                                                                                                                      documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murphy
              Vibrio cholerae Al fragment toxin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New hybrid molecules for delivery of agents binding domain of a cell binding ligand and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-AUG-1993;
                                                 15-FEB-2000
                                                                                                                                                                                                                                                                         142 TACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCATGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translocation domain of a protein
                                                                                   AAZ30661;
                                                                                                                    AAZ30661 standard;
                                                                                                                                                                                                       192
                                                                                                                                                                                                                                       46
                                                                                                                                                                                                                                                                                                         30
                                                                                                                                                                                                                                                                                           TyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaAr 46
                                                                                                                                                                                                                       gGlyThrGlnThrGlyPheValArg 54
                                                                                                                                                                                                       AGGAACTCAGACGGGATTTGTTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Fig 5A-B; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                          to: AAT91636
                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP;
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85US-0742554.
89US-0456095.
90US-0538276.
93US-0102387.
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                                                                                                                    DNA; 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other;
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alignment_block: US-09-528-682-1 x AAZ30661

Similarity: Quality:

Ratio:

25.00 1.000 100.000

Length: Gaps: Percent Identity:

100. . 00C

Align seg 1/1 to:

AAZ30661

from: 1

to: 780

30 TyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaAr

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CC protein comprising three parts: (a) the first part comprises a portion of the binding domain of a cell-binding polypeptide ligand allowing the CC hybrid protein to bind to an animal cell; (b) the second part comprises a portion of a translocation domain of a naturally occurring protein cc selected from diphtheria toxin, botulinum neurotoxin, ricin, cholera CC toxin, which translocate the third part of the across thoxin and tetanus cc toxin, which translocate the third part of the across the cytoplasmic cc membrane into the cytosol of the cell; and (c) the third part comprises cc a polypeptide entity to be introduced into the cell, which is non-native cc to the naturally occurring protein of (b). This sequence represents the cytorio cholerae toxin Al fragment gene for use in generating the hybrid co fit he invention. The hybrid molecule enables the direction of compropriate therapy to affected cells, allowing them to function properly cand allowing enetic deficiency diseases. The hybrid is especially used in creating genetic deficiency diseases, by delivering to affected cells an enzyme supplying the missing function, to supplementing cellular clavels of a particular enzyme or a scarce precursor or cofactor, to calipocytes, cancer cell, or virus infected-cells), to counteracting viral confections such as HIV, by introducing appropriate antibodies to viral constrainces such as detectable labels into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-1985;
07-JUN-1985;
22-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-AUG-1993;
07-JUN-1984;
27-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant; hybrid; binding domain; ligand; animal cell; diphtheria; translocation domain; botulinum; neurotoxin; ricin; cholera; tetanus; shiga-like toxin; pertussis; translocation; cytoplasmic membrane, HIV; cytosol; therapy; genetic deficiency disease; enzyme; co-factor; poison; adipocyte; cancer; virus; infection; antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-632431/54.
P-PSDB; AAY55890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio cholerae.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Fig 5; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the treatment of Aids and genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant DNA molecule encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SERA-) SERAGEN
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 780
 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84US-0618199.
91US-0722484.
85US-0726808.
85US-0742554.
89US-0456095.
90US-0538276.
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 243
 Α;
 130
                                                                                                                                                                                                                                                                                                                                                                                                                                        a recombinant DNA molecule encoding
Ç
 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a three part hybrid deficiency diseases
 ç;
 238
 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein used in
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CC translocation domain of a naturally occurring protein (e.g. the CC translocation domain of diphtheria toxin) the second part translocates CC the third part across the cytoplasmic membrane and into the cytosol of CC the cell. The third part comprises a chemical entity to be introduced CC into the cell, where each of the first and third part is non-native with CC respect to naturally occurring protein, and the covalent bond attaching CC the second and third part is cleavable. The toxin encoded by the present CC sequence can form part of the third portion of the hybrid protein. The CC cell binding domain binds to a specific cell and the translocation domain transfers the hybrid molecule across the cell membrane into the cytosol. CC The third part of the protein, linked to the translocation domain through care useful for treating genetic deficiency diseases by delivering to affected cells an enzyme supplying the missing function, to supplement CC cellular levels of a particular enzyme or a scarce precursor or cofactor, to direct toxins or other poisons to destroy particular cells (such as content cells, cancer cells, or virus-infected cells), and to counteract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID AAZ90017 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAZ90017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1984;
27-JUN-1991;
25-APR-1985;
07-JUN-1985;
                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the Vibrio cholerae toxin gene. The toxin be included in the hybrid protein of the invention and used to de modify the cell that the hybrid protein is targeted to. The hybrid protein comprises a first part which is a portion of the binding of a cell-binding ligand, effective to cause the hybrid molecule to a cell of an animal. The second part comprises a portion of the content of the cell of an animal of the second part comprises a portion of the cell of an animal of the second part comprises a portion of the cell of an animal of the second part comprises a portion of the cell of an animal of the cell of an animal of the cell of the cell of an animal of the cell of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cholera toxin; hybrid protein; translocation genetic deficiency disease; cell targetting; adipocyte; enzyme delivery; anti-viral; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vibrio cholerae toxin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New two-part hybrid protein comprising a translocation domain and a cell-binding domain, for treating genetic deficiency diseases, cancer and HIV infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-DEC-1989
14-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Fig 5; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SERA-) SERAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6022950-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ90017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gGlyThrGlnThrGlyPheValArg 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-160390/14.
DB; AAY78590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGAACTCAGACGGGATTTGTTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              890S-0456095
900S-0538276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91US-0722484.
85US-0726808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84US-0618199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0479510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9305-0102387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85US-0742554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA; 780 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e invention and used to destroy or is targeted to. The hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain; cell binding domain;
cell destruction; cancer;
ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                                                                                                                                                                                                   bind
            46
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alignment_block:
US-09-528-682-1 x
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
AAQ51327 standard;
toxin (CT-A) (Mekalanos et al., Nature 306, 551 (1983) - see AAQ46318; was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51327-Q51334). The invention relates to immunogenic, detoxified CT-A proteins and their use in vaccines to protect against Vibrio cholerae. Sequence AAQ51327 is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Encodes Asp-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        viral infections such as HIV by introducing into appropriate cells antibodies to viral proteins.
                                                                       The wild-type sequence coding for the A subunit of the cholera toxin (CT-A) (Mekalanos et al., Nature 306, 551 (1983) - see A
                                                                                                                          Claim 3; Fig 2 and Page 48;
                                                                                                                                                           enterotoxin
                                                                                                                                                                                                                                  P-PSDB;
                                                                                                                                                                                                                                                WPI; 1993-227320/28.
                                                                                                                                                                                                                                                                                   Domenighini M,
                                                                                                                                                                                                                                                                                                                                                       31-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                       30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUL-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9313202-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic detoxified CT-A; cholera vaccine; adenylate cyclase; protomer A; site-directed mutagenesis; reduced toxicity; ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ51327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 TACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCATGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 780 BP;
                                                                                                                                                                                               Immunogenic
                                                                                                                                                                                                                                                                                                                    (BIOC-) BIOCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 TyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAlaAr
                                                                                                                                                                               useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gGlyThrGlnThrGlyPheValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGAACTCAGACGGGATTTGTTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:AAQ51327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                  AAR44026
                                                                                                                                                         detoxified mutant cholera to vaccines against infection producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ90017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ90017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cholera
                                                                                                                                                                                                                                                                                   Hol W,
                                                                                                                                                                                                                                                                                                                                                       91IT-0MI3513
                                                                                                                                                                                                                                                                                                                                                                                         92WO-EP03016
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1.000
100.000
                                                                                                                                                                                                                                                                                                                      SCLAVO SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "wild-type GTT(Val) mutated to GAC(Asp)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 A; 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           toxin
                                                                                                                                                                                                                                                                                   Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                723 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from:
                                                                                                                          60pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169
                                                                                                                                                                                                                                                                                 Rappuoli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                               toxin and I
n by Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 T;
                                                                                                                                                                             γd
                                                                                                                                                                                                                                                                                     æ
                                                                                                                                                                                             and heat labile toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .000
                                                                                                                                                                                 cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191
                                                                       see AAQ46318)
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Section of the sectio
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US-09-528-682-1 x AAQ51327
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    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22×30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:AAQ31263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AAQ51327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     documentation_block:
AAQ31263 standard; DNA; 777
  misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation.
                                                             misc_difference
                                                                                                                       misc_difference
                                                                                                                                                                                 misc_difference
                                                                                                                                                                                                                                           misc_difference
                                                                                                                                                                                                                                                                                                     misc_difference
                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutant A subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ31263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 GAGTACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aArgGlyThrGlnThrGlyPhe 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGAGGAACTCAGACGGGATTT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          toxin; Al;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
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                                                                                                                                                                                                                                                                                      /label= A2
?33..75
                                                                                                                 /*tag= j
/note= "Argl1
184..186
                                                         /*tag= k
/note= "His44
262..264
/*tag= 1
/note= "His70 codon
388..390
                                                                                                                                                                               /note= "Asp9
85..87
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                                                                                                                                                                                                                                       /note= "Arg7 codon mutation, 79..81
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
636
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630
                                                                                                                                                                                                                                                                                                                                                               637..777
                                                                                                                                                                                                                                                                                                                                                                             /note= "first proposed authentic COOH recombinant end of A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
1..54
                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= preA
55..774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    '*tag=
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1.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                "second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B; subunit; mutation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Б
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Gaps:
Percent Identity:
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                                                                                                                                                                                                    codon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              proposed authentic COOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0:
                                                                                                                                                                                                  mutation,
                    mutation,
                                                                              mutation,
                                                                                                                                        mutation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 T;
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100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                A1 "
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alignment_block:
US-09-528-682-1 x AAQ31263
                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                       Align seg 1/1 to:
                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                          A recombinant mol. encoding an analogue of the catalytic subunit of cholera toxin (CT), where the analogue has reduced or no catalytic activity associated with CT reactogenicity is an analogue of the A region, esp. Al region, comprising a site-specific mutation in the region bounded by the codons for Metl and Arg192 or Ser194, esp. one or more of Arg1, Arg11, Asp9, His44, His70 and Glull2 (see tag h-m of Features Table). The analogue may also comprise a truncation of the C-terminal portion starting at Trp179 (see tag n of Features Table). The DNA may also encode subunit B of CT, esp. the B oligomer in
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant DNA encoding analogue of Vibrio cholerae catalytic sub-unit - useful as a vaccine for preventing cholera, has little or no catalytic activity
345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-398532/48.
P-PSDB; AAR28830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                       Sequence 777 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7-8; Page 49-50 + Fig 1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burnette WN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-1991;
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                                                    295 TCTACTTATTATATATGTTATAGCCACTGCACCCAACATGTTTAACGT
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                     97 lAsnAspValLeuGly 102
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Database length: -1841457050
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-q-/cgn2_1/USPTO_spool/US99528682/runat_18062002_082605_8796/app_query.fasta_1.299
-DB=EST -GPMT=fastap -SUFFIX=ollp2n.rst -GAPOP=4.500
-GAPEXT=0.050 -MINMATCH=0.100 -LOOPELT=0.000 -LOOPEXT=0.000
-GGAPEXT=0.050 -VGAPEXT=0.050 -XGAPOP=60.000 -YGAPEXT=60.000
-GGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
-DELOP=6.000 -DELXT=7.000 -START=1 -MATRIX=ollg0
-TRANS=human40.cd1 -LIST=1000 -DOCALIGN=200 -THR_SCORE=quality
-THR_MIN=1 -ALIGN=50 -MODE=LOCAL -OUTEMT=P50 -NORM-ext
-HAAPSIZE=500 -MILEN=0 -MODE=LOCAL -OUTEMT=950
-USER=US09528682_@CGN1_1_4416 -NCPU=6 -ICPU=3 -LONGLOG
-USER=US09528682_@CGN1_1_4416 -NCPU=6 -ICPU=3 -LONGLOG
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b_est1:AV224462
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gb_gss:BH344372
gb_est1:BI644013
gb_est1:AW523634
gb_est2:BG274791
gb_est2:BG274791
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9b_gst:AI748724

9b_est:AI859067

9b_est2:BE606331

9b_est2:BF07972

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gb_est1:AU221615
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gb_est2:H79735
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9b_est1:AV91861

9b_gss:TA194R080

9b_est2:BF517430

9b_est2:BF517430

9b_est2:BF643144

9b_gss:AQ366242

9b_gss:AQ189387
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gb_est2:BF548926
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gb_gss:AQ786225
gb_est2:BI751567
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gb_gss:BH340335
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! BE293431 600942804T2 NIH_MGC ! AZ888194 RPCI-24-168A10.TJ R	CH230-115H15.TVB CH	' ie10d03.y1 HR85 is1	CH230-187B22.TJ CHO	mw96d12 rl Soares m	RPCI-23-79110.TV RP	pqfln.pk004.fl4 nor	TCBAD2DARSS Dediatr	RC-BT122-180399-068	QV1-UT0094-121000-4	AV128660 Mus muscul) 1M0533B1BB Monse 10	3 CH230-2205.TJ CHORI	vn36d05.rl Stratage	IUM0S15H01 Liver HepG	RPCT-24-69H20 TT RP	2 1M0028I07R Mouse 10	AF094600 Mus muscul	2M0047P23R Mouse 10	946014G04 X1 946 -	3 1M0333I01R Mouse 10	? EBma05_SQ004_M17_R	RPCI-24-7106.TV RPC) sheared DNA-3564 TE	1020 Lobiolly pine C	vt14f10.rl Barstead	21 Mus musculus, clon	15 Pan troglodytes DN	11 Pan troglodytes DN	6 603061952T1 NIH_MG	31 Tetraodon nigrovir 8 602001853F1 NCT CC)7 PSR6421 ITEC PSR W	16 602101178F1 NCI_CG	Tetraodon nigroviri	Tetraodon nigroviri	Tetraodon nigroviri	Petraodon nigroviri	602941152F1 NIH_MGC	601/56489F1 NCI_CGA	1 602134766F1 NIH_MGC	727A9-Sp6.1 IGF Arabi	3 603645735F1 NIH_MGC	HVSMEh0085H01f Hord	Tetraodon nigroviri	HVSMEn0005K09f Hord	602978931F1 NCI_CGA	HVSMEi0024G08f Hord	2 AV681462 GKA HOMO S	BOGYQ44TF BOGY Bras) AV897192 Nori Satoh	MG02C06 MG Mesembry	nbxb0074L19f CUGI R	5 602420826F1 NIH_MGC	603283613F1 NIH_CGA	: BOCAW63TF BOCA Bras

9b_est1:702512 9b_est2:702512 9b_gss:AZ251059 9b_est1:AB408813 9b_est1:AW761778	gb_est1:88184349 gb_est1:AV097394 gb_est1:AV130369 gb_est2:BF963122 gb_est2:BF963122	gb_est1:AV123125 gb_est1:AW834103 gb_gss:AZ792538 gb_est1:AA710780	gb_est1:AV313935 gb_est1:AA285396 gb_gss:B75238	gb_est1:AI894283 gb_gss:CNS02B5N gb_est2:M78849 gb_est1:AV105060	gb_gss:BH220949 gb_est1:AA052073 gb_est2:BG396342	<pre>gb_est1:AV168687 gb_est1:BE070259 gb_gss:AZ401994</pre>	gb_est1:AA323391 gb_est1:AA062119	gb_est1:AW887781 gb_est1:AA914357	gb_est2:R79754 gb_est2:BE621233 gb_est1:AW566961	gb_est1:BB598038 gb_est2:BM404638	gb_est2:BG558458 qb_qss:BH323724	gb_est1:BB173809 gb_est1:AA351870 gb_gs:BU507645	gb_est1:AA380521 gb_gss:AZ889620 gb_gss:AQ357134	gb_gss:BH078864 gb_est1:AV284282	gb_est2:BF986985 gb_est2:F25852 gb_gss:BH267920	gb_est1:AU242562 gb_est2:BI012349	gb_gss:BH369347 gb_est1:AW903803	gb_est2:BI060066 gb_est1:AA787052	gb_est2:BE520222 ah_est1:AA230954	9b_est1:AV092156	gb_est1:AI382944	gb_est1:AV246346 gb_est1:AW874145	gb_est1:AV039349 gb_est1:BB046590	gb_est1:AW3243/1 gb_est1:AA870344 gh_est2:RG982311	gb_gss:BH081365 gb_est2:BF659767 gb_gss:BH266086 gb_est1:AV555670
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907 Nogawa, Miyamae-ku,
Tel: 81-44-797-2281
Fax: 81-44-797-2622
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 143)
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                                                 DNA sequence.
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31 c 27 g 37 t
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sapiens cDNA
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                                        AUTHORS
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Matsuyama,T., Miki,R.,
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Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 2
Tel: 301 838 0200
Tex: 301 838 0208
                                                                                                                                                                                                                                                                                                                                sequence.
AV224462
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1 (bases 1 to 713)

Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
              1 (bases 1 to 231)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kusakabe, M., C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Karayata M., Oda H. Okazaki V.
                                                                                                                                                           Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                extra embryonic tissue
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                                                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                   AV224462.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: hbe@tigr.org
                                                                                                                                                                                                                                                nouse mouse
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/clone="RPCI-11-347C8"
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/db_xref="GDB:7632919"
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/sex="Male"
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                                                                                                                                                           ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                      GI:6173840
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Mizuno,Y.,
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Nakamura, M., Oda, H.,
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alignment_block:
US-09-528-682-1 x AV224462/rev
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                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
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Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki.N., Izawa,M., Watahiki.M., Ozawa,K., Tanaka,T., Yoneda,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKEN Mouse ESTs (Konno, H., et al. 1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-7-22 Suehiro-cho, Tsurumi-ku, Tel: 81-45-503-9222
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                                                                                                      Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 visit our web site (http://genome.gsc.riken.go.jp) for
                                                                           9.00
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                                                                                                                                                                                                                                                                                                                               prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                            modified pBluescript KS(+) after bulk excision from Lambda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="18 days pregnant, adult"
/lab_host="DH10B"
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/clone="3830420N18"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="female"
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AL Unpublished (1999)
AL Unpublished (1999)
AL Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

Sciences Center (GSC), Yokohama Institute

Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki.N., Izawa,M., Watahiki.M.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   visit our web site (http://genome.rtc.riken.go.jp) for
/note-"Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="5430431D15"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                            /tissue_type="head"
                                                                                                                                                                                                                                                                                                 /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RIKEN full-length enriched, 6 days neonate
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su,M., Okazaki,Y. and
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Hayashizaki
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BASE COUNT ORIGIN

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alignment_block:
US-09-528-682-1 x AV292948
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                                                                                                                                                                                                                                                                                                                                                                                                                          Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Development of Barley Transcriptome Resources Unpublished (2001)
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443 bp mRNA linear EST 26-SE EBem04_SQ001_J05_R IGF Barley EBem04 library Hordeum vulgare clone EBem04_SQ001_J05 5', mRNA sequence.
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1 (bases 1 to 443)
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                                                                                                                                                                                                                                                                                                                                                          Scottish Crop Research Institute Invergowrie, Dundee, DD2 5DA, Scotland,
                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Waugh R
                                                                                                                                                                                                                                                                                                         Email: rwaugh@scri.sari.ac.uk
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/note="Vector: psporm1; Site_1: Sal I; Site_2: Not I; Non-normalised library, directionally cloned into psporm1. Derived from embryos dissected from developing grains (12 days post anthesis) in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of
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/clone="EBem04_SQ001_J05"
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/dev_stage="12 days post anthesis"
/lab_host="DH10B"
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/cultivar="Optic"
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KEYWORDS VERSION ACCESSION DEFINITION seq_name:

27

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alignment_block:
US-09-528-682-1 x AU168059/rev
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LOCUS AU168059
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61 SerThrSerLeuSerLeuArgSerAla
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National Institute of
Anagawa 4-9-1, Inage,
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(5' -> 3').
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mita, K., Ishikawa, Y. and Yamauchi, M. Establishment of cDNA database of medaka, Oryzias latipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: kmita@nirs.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
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Function) project."
170 c 96 g
                                                                                                                                                                                                                                                                         /clone_lib="01-br-ad cDNA"
/sex="female/male mixed"
/tissue_type="brain"
/dev_stage="adult"
211 c 217 g 132
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/clone="br1696"
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/strain="HNI"
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                                                                              seq_name: gb_gss:BH111124
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                                                                                                                        GGGTACGTAAGCACCAGCTTGTCCTTG
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BH111124 104 bp DNA linear GSS 19-JUL-2001 RPCI-24-367M2.TJ RPCI-24 Mus musculus genomic clone RPCI-24-367M2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

1 (bases 1 to 768)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Dean RA Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rdean@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n-7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25x genome coverage. High density colony filters are available upon request."

10 c 241 g 167 t 1 others
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/lab_host="E. coli DH10B"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
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/strain="70-15"
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/clone="mgxb0022A11r"
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US-09-528-682-1 x BH111124
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                                        KEYWORDS
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Ratio: 1.000
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18 ArgSerGlyGlyLeuMetProArg
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                                           BI778862 137 bp mRNA linear EST 26-SEP-20 EBro01_SQ001_M17_R IGF Barley EBro01 library Hordeum vulgare cDNA clone EBro01_SQ001_M17 5', mRNA sequence.
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Other_GSSs: RPCI-24-367M2.TV
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Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
BI778862.1 GI:15781754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Shaying Zhao
Department of Eukaryotic Genomics
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pletter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
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/clone="RPCI-24-367M2"
/clone_lib="RPCI-24"
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P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozame,T., Hori,F., Ishii,Y., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Ono,T., Owa,C., Saito,H., Sakai,C., Sacho,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
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All sequence has a Phred quality score of
Seq primer: M13 reverse.
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Development of Barley Transcriptome Resources
Unpublished (2001)
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 141)
Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
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Tel: 00 44 1382 562731
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
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/clone_lib="IGF Barley EBro01 library"
/tlssue_type="Root, unstressed"
/lab_host="DH10B"
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/db_xref="taxon:4513"
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64 LeuSerLeuArgSerAlaHisLeu 71
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Carninci,P. and Hayashizaki,Y. Carninci,P. and Hayashizaki,Y. Methods Enzymol. 303, 1999.
                                                                                                                                                                                                                                                                     Quality:
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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                                                                                                                                                                                                                                        Ratio:
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                                                                                                                                                                                                            8.00
1.000
100.000
                                                                            BB550100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="oviduct"
/dev_stage="2 days pregnant adult"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Site_1: Sal1; Site_2: BamHI; cDNA library was
/note="Site_1: Sal1; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5]
                                                                                                                                                                                                                                                                                                                                                                                                    pBluescript KS(+) after bulk excision from Lambda FLC I." 74 c 10 g 32 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                was cleaved with BamHI and XhoI. Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adult female oviduct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="E230020G08"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
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4 CTCTCACTCCGTTCCGCCCACCTC

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ACCESSION
VERSION
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US-09-528-682-1 x BF292752
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seq_name: gb_est2:BE517249
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Ratio: 1.000
Percent Similarity: 100.000
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                                                        34 TCGACAAGCTTGTCTCTGCGAAGT 57
                                                                                                                61 SerThrSerLeuSerLeuArgSer 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 bp mRNA linear EST 17-NOV-2000 WHE2202_D09_G18ZS Aegilops speltoides anther cDNA library Aegilops speltoides cDNA clone WHE2202_D09_G18, mRNA sequence.
BF292752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aegilops speltoides.
Aegilops speltoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooldeae;
Triticeae; Aegilops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
quality sequence with phred score less than
Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 159)
Akhunov,E., Anderson,O.D., Chao,S., Chin,A., Choi,D.W., Close,T.J., Fenton,R.D. Han,P.S., Hsia,C.C., Kang,Y., Kianian,P., Lazo,G.R., Miller,R., Otto,C., Rausch,C.J., Seaton,C.L., Simons,K., Tong,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The structure and function of the expressed portion of the wheat genomes - Anther CDNA library from Aegilops speltoides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown in a growth chamber at the University of California, Davis (Akhunov). Premeiotic anthers were harvested, total RNA and poly(A) RNA were prepared, from each tissue and then pooled, a cDNA library was made, and the CDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="WHE2202_D09_G18"
/clone_lib="Aegilops speltoides anther cDNA library"
/tlssue_type="Anther"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Aegilops speltoides"
/cultivar-"F2 from 2-12-4-8-1-1-1-(1) x PI36909-12-811-(1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="Premeiotic anthers"
/lab_host="E. coli SOLR"
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Gaps: 0
Percent Identity: 100.000
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KEYWORDS
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US-09-528-682-1 x BE517249
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seq_name: gb_est1:AA637879
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ORIGIN
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Percent Similarity: 100.000
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                                                                                  93 TCGACAAGCTTGTCTCTGCGAAGT 116
                                                                                                                                                                    SerThrSerLeuSerLeuArgSer 68
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Anderson,O.D., Chao,S., Han,P.S., Hsia,C.C., Johnson,R.R, Kang,Y.,
Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L., Tong,J.C., Verhey
,S.D. and Walker-Simmons,M.K.
The structure and function of the expressed portion of the wheat
genomes - ABA-treated embryo library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence have been trimmed to remove vector sequence and quality sequence with phred score less than 20 seq primer: Clontech Matchmaker 3' AD primer.
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West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone-Inbe-Wheat ABA-treated embryo cDNA library"
/tissue_type="Seed embryo"
/dev_stage="Mature dormant seeds"
/lab_host="E. coli DH12s"
/note="Yector: pGAD10; Site_1: EcoRI; Site_2: XhoI;
/note="Yector: pGAD10; Site_1: EcoRI; Site_2: XhoI;
/mote="Yector: pGAD10; Site_1: Coll ) in Site_1: XhoI;
/mote="Yector: pH 5.7,
/mote="Yector: ph 6.7,
/mote="Yector: p
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seq_documentation_block:

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alignment_scores:
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KEYWORDS
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                                                                                                                                          Align seg 1/1
                                                                                                                                                                                                                                    Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                 US-09-528-682-1 x AA637879
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                                                                 51
                                                                                 ThrSerLeuSerLeuArgSerAla 69
                        gb_est2:BM373106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@vatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:611437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubu. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA637879
169 bp mRNA linear EST 22-OCT-19:
vr29h03.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
IMAGE:1122101 5' similar to TR:G1020151 G1020151 CLP36. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Seq primer: -20ml3 rev2 Ef from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                          to: AA637879
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                   3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library constructed by Bob Barstead. The C2C12 cell line [available from ATCC, catalog # CRL-1772] differentiates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C3H"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
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seq_name: gb_est1:AW202162
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LOCUS BM373106
                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: BM373106
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                                                                                                                                                                                                                                                                                           61 SerThrSerLeuSerLeuArgSer 68
                                                                                   AW202162 254 bp mRNA linear EST 02-DEC-2001 sf12f04.yl Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1027-2072 5' similar to TR:Q9ZVI8 Q9ZVI8 T6A23.14 PROTEIN. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Invergowrie, Dundee, DI
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM373106 232 bp mRNA linear E EBma04_SQ003_C02_R IGF Barley EBma04 library Hordeum clone EBma04_SQ003_C02 5', mRNA sequence.
AW202162.1
EST.
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                                                            mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: rwaugh@scri.sari.ac.uk
All sequence has a Phred quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
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a 82 c 77 g 41 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="EBma04_SQ003_C02"
/clone_lib="IGF Barley EBma04 library"
/tissue_type="Maternal tissue"
/dev_stage="10 days post anthesis"
/lab_host="DH10B"
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/db_xref="taxon:4513"
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Public Soybean EST Project
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 492 Std Error: 0.00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
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                                                                                                                                               library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
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seedlings"
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/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1027-2072"
/clone_lib="Gm-c1027"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: msoares@blue.weeg.ulowa.edu
The sequence tag present in the cDNA between the NotI site and the
Oligo-GT track served to identify a clone from the normalized
adult 8-Day-Embryo library. cDNA Library Preparation: M. Fatima
Bonaldo, Ph.D. Clone distribution: clones will be available through
Research Genetics This clone is also available through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Bokstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA998803 258 bp mRNA linear EST 04-JUI-R-CO-im-h-12-0-UI-R-CO Rattus norvegicus cDNA clone UI-R-CO-im-h-12-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   discovery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I.M.A.G.E. Consortium at ID=1782402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Jun 5, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus
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Mammalia; Eutheria;
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/lab_host="DHIOB (Life Technologies)"
/lab_host="DHIOB (Life Technologies)"
/lab_host="Not I; Site_2: Eco RI; The UI-R-CO
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/lab_host="Library is a subtracted library derived from the UI-R-Al
/lab_host="Library is a subtracted library consisted of a
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/clone="UI-R-CO-im-h-12-0-UI"
/clone_11b="UI-R-CO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLNL (into@image.llnl.gov). IMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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The remaining single-stranded

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US-09-528-682-1 x AA998803/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_gss:AZ788524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A2788524 263 bp DNA linear GSS 16-FEB-200 2M0035K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0035K08 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: K column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                             Class: plasmid ends
High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                           Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606 Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Utah Genome 
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical Polymers Research Bldg., 20 S.
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                                                                                                                                                                                    /organism="Mus musculus"
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/db_xref="taxon:10090"
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                                                  Laboratory Mouse DNA Resource
                        (http://www.jax.org/resources/documents/dnares/).
                                                                                                                                             /sex="Male"
                                                                                                                                                                 /clone_lib="Mouse 10kb plasmid UUGC1M library"
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hydrodynamically sheared by
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repeated passage through
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                          The DNA
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KEYWORDS SOURCE

ORGANISM

VERSION ACCESSION

161

REFERENCE

AUTHORS

COMMENT

MEDLINE JOURNAL TITLE

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seq_documentation_block: LOCUS A0911978
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTCACCTGGCGGGACAGAGCATT 184
Library construction: Natalia S. Akopyants, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

If using this information please cite:

N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major

Friedlin strain V1 genome by shotgun sequencing 'and the Washington

University Genome Sequencing Center For information on obtaining

clone material please contact: Natalia S. Akopyants Ph.D.

(natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Akopyants, N.S., Clifton, S.W., Martin, J., Pape, D., Wylle, T., Li, L., Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Kissinger, J., Rohitt, A., Person, B., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M., Harvey, N., McCann, R., Tsagareishvili, R., Williams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M. A survey of the Leishmania major Friedlin strain VI genome by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ911978 1ine
LMAJFV1_ln09b09.yl Leishmania major FV1 random
Leishmania major genomic clone LMAJFV1_ln09b09
                                                                                                                                                                                                                                                                                                                                                 Contact: Akopyants, NS / Beverley, SM WashU Leishmania Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           profiling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 shotgun sequencing: a resource for DNA microarrays and expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leishmania major.
                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                             Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21192569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leishmania.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ911978.1 GI:6508494
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81 c 78 g 57 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.005 inch orifice at constant velocity. The sheared DN was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5
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AUTHORS
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ORGANISM
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LOCUS BF908771
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerThrSerLeuSerLeuArgSer 68
                    Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QVI&t2=QVI-UT0096-
121000-418-b06&t3=2000-10-12&t4-1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   שניאטש 275 bp mRNA linear EST 18-JAN-200
QV1-UT0096-121000-418-b06 UT0096 Homo sapiens cDNA, mRNA sequence.
BF908771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF908771.1 GI:12300229
                                                                                                                                                                                                   Tel: +55-11-2704922
                                                                                                                                                                                                                                                                         Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                    sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                Simpson, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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High quality sequence stop: 234
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                                                                                                                                                                                                                                                  Prof. Antonio Prudente 109,
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/lab_host="ToP10 (Invitrogen)"
/note="Vector: pZero-2 (Invitrogen); Site_1: EcoRV;
Genomic DNA was isolated from stationary phase cells. For
this library, DNA was sheared to give a tight size
distribution of 1-1.5kb fragments, blunt-ended with T4 DNA
polymerase, dephosphorylated with Shrimp Alkaline
phosphatase and ligated into pZero-2 vector's EcoRV site."
a 80 c 59 g 78 t
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/strain="Friedlin strain V1"
/db_xref="taxon:5664"
/clone="LMAJFV1_in09b09"
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 bp mRNA linear EST 07. zh79f01.sl Soares_fetal_liver_spleen_lNFLS_Sl Homo sapiens clone IMAGE:418297 3', mRNA sequence. w90748
                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 947 Std Error: 0.00
Seq.primer: mob.REGA+ET
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                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                          quality sequence stop: 283.
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                     /db_xref="taxon:9606"
/clone="IMAGE:418297"
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/clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                                                                  /db_xref="GDB:1326767"
                                                                                        /organism="Homo sapiens"
                                                                                                                                  Location/Qualifiers
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LOCUS BI050522
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                                                 source
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                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-GN0015-
060101-008-f04&t3=2001-01-06&t4=1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 312)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                          Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PM2-GN0015-060101-008-f04 GN0015 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
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//ab_host="DH10B (ampicilin resistant) "T3D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen lNFLS library. 1st strand cDNA was primed
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61 c 53 g 94 t 1 others
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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312 bp mRNA linear EST 26-SEP-20 EBma03_SQ001_C14_R IGF Barley EBma03 library Hordeum vulgare cDNA clone EBma03_SQ001_C14 5', mRNA sequence.
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Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
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BI781014.1 GI:15783906
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: rwaugh@scri.sari.ac.uk
All sequence has a Phred quality score
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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                                          /note="Vector: psport; Site_1: Sal I; Site_2: Not I; Non-normalised library, directionally cloned into psport1. Derived from maternal tissue dissected from developing grains (8 days post anthesis) in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating
                                                                                                                                                                                     /db_xref="taxon:4513"
/clone="EBma03_SQ001_C14"
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/clone_1ib="IGF Barley EBma03_library"
/tissue_type="Maternal tissue"
/dev_stage="8 days post anthesis"
/lab_host="DH10B"
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/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                           /organism="Hordeum vulgare"
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Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
Development of Barley Transcriptome Resources
Unpublished (2001)
Contact: Waugh R
Unit of Genomics
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All sequence has a Phred quality
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Invergowrie, Dundee, DD2 5DA, Scotland,
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/lab_host="DH10B"
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                                                        Percent Identity:
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VERSION
KEYWORDS
SOURCE
seq_name: gb_est2:BM368647
                                                                                                                                                                                      alignment_block:
US-09-528-682-1 x BF778513
                                                                                                                                                                                                                                                                                                                               alignment_scores:
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ORIGIN
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LOCUS BF778513
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                                                                                                                                                                                                                                                        Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                   216 GATGAGATCAAGCGGAGCGGCGGG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
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                                                                              14 AspGluIleLysArgSerGlyGly 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NXSI_085_F03_F NXSI (Nsf Xylem Side wood Inclined) Pinus clone NXSI_085_F03 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 323)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pinus taeda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sederoff, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ajohnson@unity.ncsu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecular Basis of Wood Formation in the Pine Megagenome
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                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NXSI (Nsf Xylem Side wood Inclined)"
/clone_lib="NXSI (Nsf Xylem Side wood Inclined)"
/tissue_type="xylem"
/cell_type="xylem"
/dev_stage="Juvenile"
/lab_host="XLI-Blue"
/lab_host="XLI-Blue"
/lab_host="XLI-Blue"
/lab_host="xxlI-Blue"
/lab_host="xxlI-Blue"
/lab_host="xxlI-Blue"
/lab_host="xxlI-Blue"
/lab_host="year old trees (three different genotypes), in three six-year old trees (three different genotypes), in the juvenile phase. These trees were induced to form side wood by bending to a 45 degree angle and tying them to the ground. Differentiating xylem was harvested from the sides of the inclined stems, and a mixture of all three genotypes was used for the library. oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI BlueScript SK vector arms. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCACGAG'."
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/strain-"Coastal plain loblolly pine from North Carolina"
/db_xref-"taxon:3352"
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KEYWORDS
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ORIGIN
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LOCUS BM368647
                                              SOURCE
                                                               KEYWORDS
                                                                                                         ACCESSION
                                                                                                                                                 DEFINITION
                                                                                                                                                                   seq_documentation_block: LOCUS AZ094117
                                                                                                                                                                                                                          seq_name: gb_gss:AZ094117
                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
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                                                                                      VERSION
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                                                                                                                                                                                                                                                                                                                                                                                          US-09-528-682-1 x BM368647
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                       ORGANISM
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                                                                                                                                                                                                                                                                      TCGACAAGCTTGTCTCTGCGAAGT 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland,
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R. Development of Barrley Transcriptome Resources Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea; Triticeae; Hordeum.
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EBem08_SQ004_D10_R IGF Barley EBem08 library Hordeum
clone EBem08_SQ004_D10 5', mRNA sequence.
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AZ094117
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                     Mus musculus
                                                                                    AZ094117.1 GI:7736160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hordeum vulgare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rwaugh@scri.sari.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  barley.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: M13 reverse.
                                              nouse mouse.
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9 9 9
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/tlssue_type="Embryo"
/dev_stage="40 days post anthesis"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="EBem08_SQ004_D10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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US-09-528-682-1 x AZ094117/rev
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LOCUS A0123154
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JOURNAL
                        AUTHORS
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                                                                                                                                                                                                                                                                                                                              gb_gss:AQ123154
                                                                                                                                                                                           HS_3095_B1_F12_MR CIT Approved Human Gen sapiens genomic clone Plate=3095 Col=23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 448 row: B column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
                  Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S.,
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 355)
                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 346)
                                                                                                                                                                         AQ123154.1 GI:3500320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                     numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               to reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.00
1.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-448B16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RPCI-23"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
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=23 Row=L, DNA sequence
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                                                                                                                                                                                                                    sequence.
                                                                                        Euteleostomi;
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                    Holzman,T.,
                                                                   Homo.
  Adams, M.D. and
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US-09-528-682-1 x AQ123154/rev
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LOCUS BI777758
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                                                                                                                                                                                                                                                                                                                                                                                                                                     BI777758 356 bp mRNA linear 1 EBro08_SQ001_O03_R IGF Barley EBro08 library Hordeum clone EBro08_SQ001_O03 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3095 row: L column. 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                            Hediey,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L., Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R. Development of Barley Transcriptome Resources Unpublished (2001)
                                                                                    Invergowrie, Dundee, DD2
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                                                                                                                                        Unit of Genomics
Scottish Crop Research Institute
                                                                                                                                                                               Contact: Waugh R
                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                   barley
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Fax: (206) 616-3887
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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                                                                     Email: rwaugh@scri.sari.ac.uk
                                                                                                                                                                                                                                                                                                                                                Hordeum vulgare
                                                                                                                                                                                                                                                                                              Triticeae;
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                              sequence has a Phred quality primer: M13 reverse.
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E-Col1 DH10B"
a 83 c 57 g 70 t
             Location/Qualifiers
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/db_xref="taxon:9606"
/clone="plate=3095 Col=23 Row=L"
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/sex="male"
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Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Waugh R Unit of Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L., Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
Development of Barley Transcriptome Resources
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                  Email: rwaugh@scri.sari.ac.uk
All sequence has a Phred quality
Seq primer: M13 reverse.
                                                                                                                                                                                                                                                                                                                                                                 Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland,
Tel: 00 44 1382 567731
Fax: 00 44 1382 562426
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/note="Vector: psport; site_1: Sal I; Site_2: Not I; Non-normalised library, directionally cloned into psport Derived from endosperm tissue dissected from developing grains (8 days post anthesis) in glasshouse grown barley
                                                                                /clone="EBed02_SQ002_O06"
/clone=11b="IGF Barley EBed02 library"
/tissue_type="Endosperm"
/dev_stage="8 days post anthesis"
/lab_host="DH10B"
                                                                                                                                                                                         /organism="Hordeum vulgare"
/cultivar="Optic"
/db_xref="taxon:4513"
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/clone=lib="IGF Barley EBro08 library"
/tlssue_type="Drought stressed root"
/lab_host="DH10B"
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/cultivar="Optic"
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                       US-09-528-682-1 x C60468
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Percent Similarity: 100.000
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C60468 Yuji Kohara unpublished cDNA Caenorhabditis elegans
clone yk208all 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                              Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 81-559-81-6855
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 360)
1 (bases 1 to 360)
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Expression map of the C.elegans genome
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                                                                                                                                                                                                                                                                                                                                                                                  Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
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123 c 112 g 61 t
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                                                                     AUTHORS
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                                                                                                                                                                                                           360 bp
CELK059GZF Yuji Kohara unpublished
clone yk59g12 5', mRNA sequence.
D69091
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 360)
Kohara, Y., Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A., Sano
, M., Miyata, A. and Nishigaki, A.
Expression map of the C.elegans genome
                                                                                 Caenorhabditis elegans.
Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
L (bases 1 to 360)
Toward an expression map
Unpublished (1994)
Contact: Yuji Kohara
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
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Contact: Yuji Kohara
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EST.
                                                                                                                                                                                             D69091.1 GI:1104744
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Location/Qualifiers
                                                                   Kohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T.,
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/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
71 c 77 g 107 t
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/db_xref="taxon:6239"
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LOCUS AW740520
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Genes expressed by the hemocytes of Biomphalaria glabrata before and after exposure to miracidia Unpublished (2000)
Contact: Raghavan N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW/40520 363 bp mRNA linear EST 27-APR-2000 BRI10477 Biomphalaria glabrata (BS-90)-unexposed Lambda Zap Library Biomphalaria glabrata cDNA clone RBGIG25TR, mRNA sequence. AW740520
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Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biomphalaria glabrata
                                                                                                                                                                                                                                                                                                               Tel: 301-881-3300 ext.128 Fax: 301-770-4756
                                                                                                                                                                                                                                                                                                                                                  Biomedical Research Institute
12111 Parklawn Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bloodfluke planorb
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                                                                                                                                                                                                                                                                     nkr@helix.nih.gov, snailsrule@aol.com.
Location/Qualifiers
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Location/Qualifiers
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                                                                                                                                             /organism="Biomphalaria gl
/strain="BS-90"
/db_xref="taxon:6526"
/clone="RBGIG25TR"
/clone=lib="Biomphalaria g
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1.000
/cell_type="Hemocyte"
/lab_host="Laboratory host"
/lab_host="Laboratory host"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Total RNA was isolated from the hemocytes of
XhoI; Total RNA was isolated from the hemocytes of
XhoI; Total RNA was isolated from the hemocytes of
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                                                                                                                              Zap Library"
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/strain="CB1489 him=8(e1489)"
/db_xref="taxon:6239"
/clone="yk59g12"
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alignment_scores:

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US-09-528-682-1 x AW740520/rev
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ORIGIN
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Ratio: 1.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerThrSerLeuSerLeuArgSer 68
                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC, Hood I
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, W7
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3054 row: D column: 13
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUUYYYBA 369 bp DNA linear GSS 27-AUG-1998
HS_3054_Bl_B07_MF CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3054 Col=13 Row=D, DNA sequence.
AQ099964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 369)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Kaller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ099964.1 GI:3470993
GSS.
                                                                                                                                                                                                                           High quality sequence stop: 369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping
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                   /note="Organ: sperm; Vector:
E-Coli DH10B"
a 100 c 64 g 127 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strand cDNA synthesized using an oligo-dT primer-linker (XhoI). Second strand synthesis was followed by the ligation of EcoRI adaptors. Following digestion with XhoI, the completed, directional cDNA was cloned into Uni-ZAP XR Phagemid vector by Stratgene.
                                                                           /clone="Plate=3054 Col=13 Row=D"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                    1. .369
                                                                                                                                                                                                     ocation/Qualifiers
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US-09-528-682-1 x AQ099964
    seq_documentation_block:
LOCUS H78351
                                                            seq_name: gb_est2:H78351
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US-09-528-682-1 x AQ544348
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ORIGIN
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LOCUS A0544348
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                                                                                                                                                                                                                                                                                      Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                       Align seg 1/1 to: AQ544348
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                                                                                                                          ValSerAlaLeuGlyGlyIlePro 120
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                                                                                                       GTATCTGCTTTAGGAGGCATCCCA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
Other_GSSs: CITBI-E1-2651G15.TF
Other_GSNs: CITBI-E1-2651G15.TF
Contact: Shaying Zhao, William Nierman,
Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITBI-E1-2651G15.TR CITBI-E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Map Building
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
a 65 c 80 g 146 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2651G15"
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Homo sapiens genomic clone 2651G15,
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LOCUS AZ081963 372 bp
DEFINITION UP_566-2E_T7 RPCIll Human Male BAC
clone 566-2E, DNA sequence.
                                           seq_documentation_block:
LOCUS AZ081963
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Quality:
                                                                                                   seq_name: gb_gss:AZ081963
                                                                                                                                                                                                                                                                            US-09-528-682-1 x H78351
                                                                                                                                                                                                                                                                                                                                      Percent Similarity: 100.000
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1 (bases 1 to 372)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J. Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yu79f12.rl Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:240047 5', mRNA sequence.
H78351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; MAGE Consortium (info@image.llnl.gov) for further i Insert Length: 692 Std Error: 0.00 Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
Insert Size: 692
High quality sequence stops: 236
Source: IMAGE.Consortium, LLNL
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Contact: Wilson RK
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Fax: 314 286 1810
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/db_xref="GDB:3789000"
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US-09-528-682-1 x AZ081963/rev
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LOCUS BH462450
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Ratio: 1.000
Percent Similarity: 100.000
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Brassica oleracea.

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec

Eukaryota; Viridiplantae; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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University of Pennsylvania
3516 Civic Center Blvd, ARC 516, Philadelphia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheung, V.G., Dalrymple, H.L., Narasimhan, S., Watts, J., Schuler, G., Raap, A.K., Morley, M. and Bruzel, A. A resource of mapped human bacterial artificial chromosome clones Genome Res. 9 (10), 989-993 (1999)
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AZ081963.1
                                                                      Whole genome shotgun sequencing Unpublished (2001) Other_GSSs: BOHKZ35TR
                                                                                                                                                                                                                                                          GSS
                                                                                                                                                                                                                                                                                          Sequence.
BH462450
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Plate: 566 row: E column: 2
Seq primer: T7
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                                                                                                        Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea
                                                                                                                                                                                                                                                                         BH462450.1 GI:17654289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 215 590 2664 Fax: 215 590 3709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Arcaro MA, Morley M, Burdick J,
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                                                       Contact: Chris Town
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                                                                                                                                            (bases 1 to 381)
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Medical Center Drive, 301-838-3523
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/db_xref="taxon:9606"
/clone="566-2E"
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/cell_type="Lymphocytes"
/note="Vector: pBACe3.6;
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                 Rockville,
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alignment_block:
US-09-528-682-1 x BH462450/rev
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                                                                                                                                                                                                                                                                                                                                                                              Contact:
Dept. of
                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

[ (bases 1 to 382)

White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de
Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C.
A new set of Arabidopsis expressed sequence tags from developing
seeds. The metabolic pathway from carbohydrates to seed oil
plant, Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M21C8STM Arabidopsis clone M21C8 5', mRNA BE521751
                                                                                                                                                                 Michigan State University DNA Sequencing Facility Arabidopsis Biological Resource Center, The Ohio State University, 309 Bor Zoology Bidg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX: 6142920603 TEL: 6142929371.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cdtown@tigr.org
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                                                                                                                                                                                                                                                                        Tel: 517 355 1609 Fax: 517 353 9334
                                                                                                                                                                                                                                                                                                                                                        Michigan
                                                                                                                                                                                                                                                    Email: benning@msu.edu
                                                                                                                                                                                                                                                                                                                                     224 Biochemistry, Michigan State University, East Lansing, MI 48824
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State University
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI linkers"
genomic DNA inserted into pHOS1 using BstXI linkers"
a 73 c 82 g 91 t
                                                                                                                                                                                                                                                                                                                                                                                                  Benning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHKZ35"
                                                                                  /organism="Arabidopsis
/strain="Columbia"
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/clone_lib="Arabidopsis developing seed"
/tissue_type="seed"
                                         /db_xref="taxon:3702"
/clone="M21C8"
                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Johnson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
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Fax: 919 515 7801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            il: ajohnson@unity.ncsu.edu
primer: T3.
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                           77
                 /note="vector: BlueScript SK; Site_1: Eco RI; Site_2: XhoI; The library is from early (spring) wood, taken from three six-year old trees (three different genotypes), in the juvenile phase. These trees were induced to form compression wood by bending to a 45 degree angle and tying them to the ground. Differentiating xylem was harvested from the bottoms of the inclined stems, and a mixture of all three genotypes was used for the library. oligo-dr primed cDNA was directionally cloned into the EcoRI-xhoI BlueScript SK vector arms. NOTE: The sequences contain a 'CDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCACGAG'."
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/lab_host="E.coli".
/note="organ: Developing seed; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoII"
a 90 c 87 g 86 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Pinus taeda"
/strain="Coastal plain loblolly pine from
/db_xref="taxon:3352"
                                                                                                                                                                                                                                                                                                                               /tissue_type="Xylem"
/cell_type="Compression"
/dev_stage="Juvenile"
/lab_host="XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                           /clone="NXCI_086_C11"
/clone_lib="NXCI (Nsf xylem Compression wood Inclined)"
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Quality: 8.00
Ratio: 1.000
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The Washu-Merck EST Project
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393 bp mRNA linear EST 17-OCT-1996 zd79g08.sl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346910 3', mRNA sequence.
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 671_ Std Error: 0.00
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4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                       /dev_stage="19 weeks"
//dev_stage="19 weeks"
//lab_host="bHlOB (ampicillin resistant)"
//lab_host="bHlOB (ampicill
                               same fetus as the fetal lung NbHL19W." 87 c 69 g 114 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:1272285"
/db_xref="taxon:9606"
/clone="IMAGE:346910"
/clone_1ib="Soares_fetal_heart_NbHH19W"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         School of Medicine way, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
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                                                                                                               library, Soares fetal lung
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JOURNAL COMMENT
                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
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KEYWORDS
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US-09-528-682-1 x AQ114866/rev
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US-09-528-682-1 x W78167/rev
                                                                                                                                                                                                                                alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_gss:AQ114866
seq_name: gb_gss:AQ120888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                Align seg 1/1 to reverse of: AQ114866
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                                  367
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                                GTATCTGCTTTAGGCGGCATCCCA 344
                                                               ValSerAlaLeuGlyGlyIlePro 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seq primer: M13 Reverse Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1998)
Other_GSSs: CIT-HSP-2375K8.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ114866
AQ114866.1 GI:3490987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIT-HSP-2375K8.TR CIT-HSP Homo sapiens genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams, M.D., Rounsley, S.D., Zha
Berry, K., Granger, D., Suh, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 395)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of a random human BAC End Sequence Database for
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                                                                                                                                                                                                                                                                                                   102
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                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2375K8"
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                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="CIT-HSP"
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Gaps:
Identity:
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E., Wible,C., Shizuya,H., Simon,M. and
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e 2375K8, DNA
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KEYWORDS
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AUTHORS
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LOCUS BF908074
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US-09-528-682-1 x AQ120888/rev
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                          AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 398)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R. Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A0120888 396 bp DNA linear GSS 22-SEP-1998 HS_3073_B1_C01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=1 Row=F, DNA sequence.
A0120888 ADDITIONAL SERVICE S
                                                                                                                                                                                                                                                                                                                                                            BF908074 398 bp mRNA lin
RC1-UT0083-091000-013-f01 UT0083 Homo sapiens
BF908074
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Plate: 3073 row: F column: 1
Plate: 3073 row: F column: 1
Class: BAC ends
High quality sequence stop: 396.
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GSS.
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
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                                                                                                                                                                                                                                                          human.
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E-Coli DH10B"
a 93 c 74 g 80 t 4 others
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/sex="male"
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/db_xref="taxon:9606"
/clone="plate=3073 Col=1
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                                                                          Briones, M.R.,
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US-09-528-682-1 x BF908074/rev
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LOCUS AW587771
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                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_est1:AW587771
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Ratio:
                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 400)

Whetten,R.W., Kinlaw,C.S., Retzel,E. and Sederoff,R.R.

The Pine Gene Discovery Project
Unpublished (1999)
Contact: Ross Whetten
Forest Biotechnology Group
                                                                                                                                                                                                                                                                                                               400 bp
ST66F07 Pine TriplEx shoot tip 1
ST66F07, mRNA sequence.
AW587771
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-UT0083-091000-013-f01&t3=2000-10-09&t4=1)
Seq primer: puc 18 forward
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Shotgun sequencing
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Location/Qualifiers
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Ludwig Institute for Cancer Research
Ludwig Prof. Antonio Prudente 109, 4 andar, 01509-010,
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                                                                                                                                                                                                                                             loblolly pine.
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+55-11-2707001
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Carolina State University of Forestry, NC State University, 6113 Jordan Hall, Raleigh
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100.000
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-NN1025-100
500-183-b01&t3=2000-05-10&t4=1)
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QV3-NN1025-100500-183-b01 NN1025 Homo
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Tel: 919-515-7800
Fax: 919-515-7801
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Ludwig Institute for Cancer Research
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                                                                                                                        Fax: +55-11-2707001
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primer: 5' lambda TriplEx2
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/(lab host="E. coli BM25.8"
/(lab host="E. coli BM25.8"
/(lab host="E. coli BM25.8"
/(note="Organ: shoot tips; Vector: Lambda TriplEx; Site_1: SfiI (A); Site_2: SfiI (B); Shoot tips (approx. 2 cm from apex) were collected during the spring, frozen and used for mRNA isolation. The SMART-PCR method (Clontech) was used to prepare a library from 1 ug total RNA, using the Lambda TriplEx vector. Plasmid subclones in pTriplEx were recovered by cre-lox excision in E. coli strain BM25.8 and sequenced from the 5' end."
81 a 98 c 110 g 97 t 14 others
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/db_xref="taxon:3352"
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Ratio: 1.000
Percent Similarity: 100.000
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AI350210
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                                                                                                                                                    cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 566 Std Error: 0.00
Seq primer: -40Up from Gibco
High quality sequence stop: 379.
Location/Qualifiers
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1 (bases 1 to 408)
                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                          Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
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Site_2: SmaI; A min1-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
/clone_lib~"NCI_CGAP_Lu5"
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/lab_host-"DH10B"
                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1910298"
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/dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est2:BF777429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
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Ratio: 1.000
Percent Similarity: 100.000
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410 bp mRNA linear EST 12-JAN-2001 NXSI_071_E05_F NXSI (Nsf xylem Side wood Inclined) Pinus taeda cDNA colone NXSI_071_E05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Johnson, Arthur
North Carolina State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 410)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 919 515 7800
Fax: 919 515 7801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pinus taeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ajohnson@unity.ncsu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular Basis of Wood Formation in the Pine Megagenome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sederoff, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oblolly pine.
                                                                                                                                                                                                                                                                                                                                                                                                                                      primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163
 81
                              /note="Organ: lung; Vector: pT/TT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. " a 62 c 61 g 122 t
adapter sequence is
                                                                                                                                                                                                                                                                     /tissue_type="Xylem"
/cell_type="Side"
                                                                                                                                                                                                                                                                                                       /strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="MXSI_071_E05"
/clone_11b="NXSI_(Nsf Xylem Side wood Inclined)"
                                                                                                                                                                                                                                                                                                                                                                                 ∕organism="Pinus taeda"
                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                      'dev_stage="Juvenile"
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ORIGIN

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BASE COUNT
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AUTHORS
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US-09-528-682-1 x BF777429
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ORGANISM
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LOCUS BH340335
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Ratio: 1.000
Percent Similarity: 100.000
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    Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CH230-183D15.TV CHORI-230 Segment 1 CH230-183D15, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 183 row: D column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Other_GSSs: CH230-183D15.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                          Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH340335.1 GI:17271069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 415)
                                                                                                                          132
                                                                                                                     Pieter de Jong"
1 108 c 73 g
                                                                                                                                                           /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI; CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shaying Zhao
    8.00
1.000
                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .415
                                                                                                                                                                                                                            /sex="Female"
                                                                                                                                                                                                                                                                                     /strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
                                                                                                                                                                                                     cell_type="Brain"
                                                                                                                                                                                                                                             /clone_lib="CHORI-230 Segment 1"
                                                                                                                                                                                                                                                                  /clone="CH230-183D15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences from Library CHORI-230 EcoRI segment
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Gaps:
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US-09-528-682-1 x BH340335/rev
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1M0568F17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0568F17 R, DNA sequence.
A2768672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0568 row: F column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 417.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
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Unpublished (20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 417)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse whole genome scaffolding with paired end reads from 10kb
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adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                             adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a book of inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="UUGC1M0568F17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (2000)
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-YGAPEXT=60.000 -FGAPOP=6.000 -DELEXT=7.000 -YGAPOP=60.000

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702-134-9229 -
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US-09-724-315-4
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US-09-528-682-1 x US-09-724-315-4
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Ratio: 1.000
Percent Similarity: 100.000
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GENERAL INFORMATION:
APPLICANT: HAYNES, Joel R.
APPLICANT: ARRINGTON, JOSHUA
TITLE OF INVENTION: NUCLEIC ACID ADJUVANTS
FILE REFERENCE: APF41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 4
LENGTH: 5500
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CURRENT FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4037 TCTTATGCCCAGAGGGCATAATGAGTACTTCGATAGAGGAACTCAAATGA 4086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 snileAsnLeuTyrAspHisAlaArgGlyThrGlnThrGlyPheValArg
                                                                                                                                                                                                                                                                                                                                                                            71 uAlaGlyGlnSerIleLeuSerGlyTyrSerThrTyrTyrIleTyrVali 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 TyrAspAspGlyTyrValSerThrSerLeuSerLeuArgSerAlaHisLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 yLeuMetProArgGlyHisAsnGluTyrPheAspArgGlyThrGlnMetA 38
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APPLICANT: HAXNES, Joel R.
APPLICANT: ARRINGTON, JOSHUA
TITLE OF INVENTION: NUCLEIC ACID ADJUVANTS
FILE REFERENCE: APF41
CURRENT APPLICATION NUMBER: US/09/724,315
CURRENT FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 5488
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US-09-528-682-1 x US-09-724-315-6
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Ratio:
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77
                                                                                                                                                                                                            27 HisAsnGluTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAs
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Percent Identity:
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APPLICANT: Boyce Thompson Institute for Plant Research at Cor
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Exp
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                      Quality: 184.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                      Align seg 1/1 to: PCT-US99-30747-3
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                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: E. coli OTHER INFORMATION: heat-labile toxin gene mutagenized to opti OTHER INFORMATION: expression in plants.
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LOCATION: (3)..(782)
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                                                                 LeuTyrArgAlaAspSerArgProProAspGluIleLysArgSerGlyGl
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seq_documentation_block:
    Sequence 3, Application US/09470124
; GENERAL INFORMATION:
; APPLICANT: Mason
; APPLICANT: Mason
; APPLICANT: ATTICE
; TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins
; TITLE OF INVENTION: Transgenic Plants
; FILE REFERENCE: 4868/84454
; OTHER INFORMATION: Description of Artificial Sequence:E.; OTHER INFORMATION: heat-labile toxin gene mutagenized to; OTHER INFORMATION: expression in plants.
US-09-470-124-3
                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/2/pna/US094_COMB.seq:US-09-470-124-3
                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/470,124
CURRENT FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 782
                                                               FEATURE:
NAME/KEY: CDS
LOCATION: (3)..(782)
FEATURE:
                                                                                                                            TYPE: DNA
ORGANISM: Artificial
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alignment_scores:
Quality:

Percent Similarity:

Ratio:

184.00 1.000 100.000

Percent Identity:

100.000

Length:

alignment_block: US-09-528-682-1 x US-09-470-124-3

US-09-470-124-3

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US-09-950-335A-5
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                                                                                                    Sequence 5, Application US/09950335A
GENERAL INFORMATION:
APPLICANT: HONE, DAVID M.
TITLE OF INVENTION: GENETICALLY ENGINEERED CO-EXPRESSION DNA VACCINES, CONSTRUCTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 4115-128
CURRENT APPLICATION UNBER: US/09/950,335A
CURRENT FILING DATE: 2001-09-10
                                                        SEQ ID NO 5
                                                                       CURRENT FILING DATE: 2001-09-10 NUMBER OF SEQ ID NOS: 23 SOFTWARE: PatentIn version 3.1
           TYPE: DNA
ORGANISM: Escherichia
                                           LENGTH: 723
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08256003 GENERAL INFORMATION:
TELEPHONE: (510) 601-2708
TELEPHONE: (510) 601-2708
TELEPHONE: (510) 601-2708
TELEPHONE: (510) 601-2708
                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDLIM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                          CURRENT APPLICATION DATA: US
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                 STREET: 4560 Horton
CITY: Emeryville
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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Pizza, Mariagrazia
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Cholera Toxin and of the Toxin Lt, Their Preparation
Their Use for the Preparation of Vaccines
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and

INFORMATION FOR SEQ ID NO:

<u>ა</u>

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; NAME/KEY: CDS
; LOCATION: 1..711
US-08-256-003-5
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                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/pna/US090_COMB.seq:US-09-044-696-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-528-682-1 x US-08-256-003-5
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                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09044696 GENERAL INFORMATION:
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BARCHFELD, GAIL
APPLICANT: DEL GIUDICE, GIU
APPLICANT: RAPPUOLI, RIO
                                                                                                                                                                                                                                                                                                                                                                                                                                     545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         TITLE OF INVENTION: DETOXIFIED MUTANTS OF BACTERIAL TITLE OF INVENTION: ADP-RIBOSYLATING TOXINS AS PARE: NUMBER OF SEQUENCES: 4
                                                                                                                                        STREET: P.O. BOX 8097
CITY: EMERYVILLE
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                          COUNTRY:
                                                                                                                                                                                        ADDRESSEE: CHIRON CORPORATION, INTELLECTUAL PROPERTY ADDRESSEE: R440
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGAATATAGCTCCGGCAGAGGATGGTTACAGATTAGCAGGTTTCCCACC
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                                                                                                              94662-8097
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US/09/044,696
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Gaps: 0
Percent Identity: 100.000
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                              Version #1.30
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 1.000 Percent Similarity: 100.000
TITLE OF INVENTION: GENETICALLY ENGINEERED CO-EXPRESSION DNA VACCINES, CONSTRUCTION TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 4115-128
CURRENT APPLICATION UNMBER: US/09/950,335A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 2
                                                                                                                                                              Sequence 2, Application US/09950335A GENERAL INFORMATION:
APPLICANT: HONE, DAVID M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-528-682-1 x US-09-044-696-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 711 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60
FILING DATE: 21-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: HARBIN, ALISA A.
REGISTRATION NUMBER: 33,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 655-8730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 LeuAsnIleAlaProAlaGluAspGlyTyrArgLeuAlaGlyPheProPr 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395 ATGAACGATTACATCGTAACAGGGAATATAGAGACCGGTATTACAGAAAT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                           lyCysGly 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCATATTCTCAGATATATGGATGGTATCGTGTTAATTTTGGTGTGATTG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGAATATAGCTCCGGCAGAGGATGGTTACAGATTAGCAGGTTTCCCACC 494
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Percent Identity: 100.000
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alignment_block:
US-09-528-682-1 x US-09-950-335A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
; LOCATION:
US-08-256-003-7
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Ratio: 1.000
Percent Similarity: 100.000
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TYPE: DN
                                                                                                                                                                                                     TELEFAX: (510 (655-354 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,003
                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 601-2708
                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0315.001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Immunogenic Detoxified Mutants of TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation and TITLE OF INVENTION: Their Use for the Preparation of Vaccines
                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 AAGAGGAACTCAGACGGGATTTGTTAGG 162
                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 aArgGlyThrGlnThrGlyPheValArg 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 GluTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAl 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Emeryville
STATE: California
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 11-NOV-1994
CLASSIFICATION: 435
                                       NAME/KEY:
                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                     STRANDEDNESS:
                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94608-2916
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                                                                                                                                                                                                                           : (510) 601-2708
(510 (655-3542
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Pizza, Mariagrazia
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                                                                                                    linear
                                                                              DNA (genomic)
                                                                                                                       double
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Gaps: 0
Percent Identity: 100.000
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alignment_scores:

alignment_scores:

Quality:

26.00

Length:

26

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-044-696-3
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/041
FILING DATE: 21-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: HARBIN, ALISA A.
REFERENCE/DOCKET NUMBER: 139:
REFERENCE/DOCKET NUMBER: 139:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 655-8730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION
                                                                                                                                                                                                                                                     TELEFAX: (510) 655-3542 INFORMATION FOR SEQ ID NO: 3:
                FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: UFILING DATE: 18-MAR-JCLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BARCHFELD, GALL
APPLICANT: DEL GIUDICE, GI
APPLICANT: RAPPUOLI, RINO
APPLICANT: REPONY
                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 AAGAGGAACTCAGACGGGATTTGTTAGG
                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 aArgGlyThrGlnThrGlyPheValArg 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: EMERYVILLE
STATE: CALIFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 GAGTACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCATGC 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: CHIRON CORPORATION, INTELLECTUAL PROPERTY ADDRESSEE: R440
                                                                           LOCATION:
                                                                                           NAME/KEY:
                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                          nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09044696
                                                                                                                                                                                                            723 base pairs
                CDS
1..720
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                                                                           misc_feature
1..720
                                                                                                                                                        linear
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Percent Identity: 100.000
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alignment_block:
US-09-528-682-1 x US-09-950-335A-1
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; ORGANISM: Vibrio cholerae
US-09-950-335A-1
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US-09-528-682-1 x US-09-044-696-3
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Ratio: 1.000
Percent Similarity: 100.000
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                                                          Sequence 45, Application PC/TUS9930747
GENERAL INFORMATION:
APPLICANT: Boyce Thompson Institute for Plant Research at CorTITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4668/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
RUMBER OF SEQ ID NOS: 67
SOCTWARE: Patentin Ver. 2.1
SEQ ID NO 45
LENGTH: 777
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APPLICANT: HONE, DAVID M.
APPLICANT: HONE, DAVID M.
TITLE OF INVENTION: GENETICALLY ENGINEERED CO-EXPRESSION DNA VACCINES, CONSTRUCTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 4115-128
CURRENT APPLICATION NUMBER: US/09/950,335A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 1
LENGTH: 723
TYPE: 723
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FEATURE:
                   ORGANISM: Artificial Sequence
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                                              DNA
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Percent Identity: 100.000
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; OTHER INFORMATION: Description of Artificial Sequence:V. cholerae; OTHER INFORMATION: cholera toxin gene mutagenized to optimize; OTHER INFORMATION: expression in plants.

PCT-US99-30747-45
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Quality:
seq_name: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:PCT-US99-30747-49
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; Sequence 47, Application PC/TUS9930747
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Percent Similarity:
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
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TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
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                                             189 AAGGGGAACTCAAACTGGATTTGTGAGG 216
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                                                                                    45 aArgGlyThrGlnThrGlyPheValArg 54
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Percent Identity:
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Percent Similarity: 100.000

Percent Identity: 100.000

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alignment_block:
US-09-528-682-1 x PCT-US99-30747-49
                                                 alignment_scores:
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OTHER INFORMATION:
OTHER INFORMATION:
PCT-US99-30747-51
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Ratio: 1.000
Percent Similarity: 100.000
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APPLICANT: Boyce Thompson Institute for Plant Research at Cor
APPLICANT: Boyce Thompson Institute for Plant Research at Cor
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 51
LENGTH: 777
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APPLICANT: Boyce Thompson Institute for Plant Research at Cor
APPLICANT: Boyce Thompson Institute for Plant Research at Cor
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed
TITLE OF INVENTION: Transgenic Plants
TILE REFERENCE: 4668/86427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 49
LENGTH: 777
TYPEF: NUMB
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ORGANISM: Artificial Sequence
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LOCATION: (1)..(777)
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LOCATION: (1)..(777)
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Quality:
Ratio:
                                                                                                                                                  Description of Artificial Sequence:V. cholerae cholera toxin gene mutagenized to optimize expression in plants.
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alignment_block:
US-09-528-682-1 x PCT-US99-30747-51
seq_documentation_block:
; Sequence 1, Application US/08435605
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Quality:
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US-07-694-733-1
                                                       seq_name: /cgn2_6/ptodata/2/pna/US084_COMB.seq:US-08-435-605-1
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microsoft Word Version 5.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/694,733 FILING DATE: 19910502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Burnette, W. Neal APPLICANT: Kaslow, Harvey R. APPLICANT: Kaslow, Harvey R. TITLE OF INVENTION: Recombing TITLE OF INVENTION: Cholera
                                                                                                                                                                               139 GAGTACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCATGC
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                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 777 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Apple M
OPERATING SYSTEM:
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STREET: 1840 Dehavilland Drive
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                                                                                                                                                                                                                                                             to: US-07-694-733-1 from: 1
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Percent Identity: 100.000
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GENERAL INFORMATION:

APPLICANT: Burnette, W. Neal APPLICANT: Kaslow, Harvey R.

TITLE OF INVENTION:

Recombinant DNA-derived Cholera Toxin

NUMBER OF SEQUENCES:

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alignment_block:
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           APPLICANT: Mason
APPLICANT: Mason
APPLICANT: Arntzen
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/84454
CURRENT ENLING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 45
LENGTH: 777
TYPE: DNA
TYPE: 
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microcoft
CURRENT And
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FILING DATE: 02-MAY-1991
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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APPLICATION NIMBERS
FEATURE:
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PRIOR APPLICATION DATA:
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TYPE: nucleic acid
STRANDEDNESS: double stranded
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STATE: California
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STREET: 1840 Dehavilland Drive
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Ratio:
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alignment_block:
US-09-528-682-1 x US-09-470-124-47
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US-09-528-682-1 x US-09-470-124-45
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US-09-470-124-45
seq_name: /cgn2_6/ptodata/2/pna/US094_COMB.seq:US-09-470-124-49
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US-09-470-124-47
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CURRENT FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 47
LENGTH 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 47, Application US/09470124
GENERAL INFORMATION:
APPLICANT: Mason
APPLICANT: Arntzen
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/84454
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TYPE: DNA
ORGANISM: Artificial Sequence
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LOCATION: (1)..(777)
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                                         189 AAGGGGAACTCAAACTGGATTTGTGAGG 216
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                                                                                   45 aArgGlyThrGlnThrGlyPheValArg 54
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OTHER INFORMATION: Description of Artificial Sequence:V. cholerae; OTHER INFORMATION: Cholera toxin gene mutagenized to optimize OTHER INFORMATION: expression in plants.
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US-09-470-124-49
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US-09-528-682-1 x US-09-470-124-49
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TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/84454
CURRENT APPLICATION NUMBER: US/09/470,124
CURRENT FILING DATE: 199-12-24
NUMBER OF SEO ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEO ID NO 49
LENGTH: 777
TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Mason
APPLICANT: Arntzen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 51, Application US/09470124 GENERAL INFORMATION:
                                                                                                                                                                                                                                                          SEQ ID NO 51
                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed In TITLE OF INVENTION: Transgenic Plants FILE REFERENCE: 4868/84454 CURRENT APPLICATION NUMBER: US/09/470,124 CURRENT FILING DATE: 1999-12-24 NUMBER OF SEQ ID NOS: 67 SOFTMARE: Patentin Ver. 2.1
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APPLICANT: Arntzen
                                                                                                                                                                                                                LENGTH: 77
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LOCATION: (1)..(777)
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                                                                                                           NAME/KEY: CDS
LOCATION: (1)..(777)
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Percent Identity: 100.000
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seq_documentation_block:
; Sequence 12, Application US/08674895
; GENERAL INFORMATION:
                                                                       seq_name: /cgn2_6/ptodata/2/pna/US086_COMB.seq:US-08-674-895-12
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                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
Quality:
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Ratio: 1.000
Percent Similarity: 100.000
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US97/11719
FILING DATE: 03-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/674,895
FILING DATE: 03-JUL-1996
INFORMATION FOR SEQ ID NO: 12:
                                                                                                        MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: IMPORTANT OF INVENTION: CONTINUES OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189
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LENGTH: 1956 base pair:
TYPE: nucleic acid
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ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 GAGTACTTTGACAGGGGTACTCAGATGAACATCAACCTTTATGACCATGC 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
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Percent Identity:
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Identity:
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alignment_block:
US-09-528-682-1 x US-08-674-895-12
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Quality:
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                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:PCT-US01-08582-1
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                        Sequence 1, Application PC/TUS0108582
GENERAL INFORMATION:
APPLICANT: UAB Research Foundation
TITLE OF INVENTION: Chimeric Nontoxic Mutants of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (619) 554-631
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                            1103
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/01
FILING DATE: 03-JUN-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: IMMUNOCONTRACEPTION COMPOSITIONS TITLE OF INVENTION: CONTAINING SPERM ANTIGEN, AND ME'S NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE:
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TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: California
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                               aArgGlyThrGlnThrGlyPheValArg 54
                                                                                                                                                                                                                                                            AAGAGGAACTCAGACGGGATTTGTTAGG 1130
                                  CORRESPONDENCE ADDRESS:
                                                      NUMBER OF SEQUENCES:
STREET: P.O. Box 2509
                 ADDRESSEE:
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                 Hendricks and Assoc
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                                                                         Humoral Immunity
                                                                                         Enterotoxins as Mucosal
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100.000
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                                                                                         Adjuvants for Cell-Mediated
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                                                                                       or.
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seq_name: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:PCT-US01-08582-2
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Quality:
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GENERAL INFORMATION:
APPLICANT: UAB Research Foundation
TITLE OF INVENTION: Chimeric Nontox
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TELECOMUNICATION INFORMATION:
TELEPHONE: 703/425-8405
TELEPHAX: 703/425-8406
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2022 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               656 GAGTACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCATGC
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US01/08582
APPLICATION NUMBER: PCT/US01/08582
FILING DATE: 16-Mar-2001
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REGISTERATION NUMBER: 32,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 GluTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAl 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 aArgGlyThrGlnThrGlyPheValArg 54
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown MOLECULE TYPE: DNA (gen HYPOTHETICAL: NO ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                  COUNTRY: US
ZIP: 22031
                                                                                                                                                          CITY: Fairfax
STATE: VA
                                                                                                                                                                                                  ADDRESSEE: Hendricks and Assoc STREET: P.O. Box 2509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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        Version #1.25
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alignment_block:
US-09-528-682-1 x US-09-724-315-3
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    Quality:
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; LENGTH: 5488
; TYPE: DNA
; ORCANISM: plasmid pPJV2006
US-09-724-315-3
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; SEQUENCE DESCRIPTION: SEQ ID PCT-US01-08582-2
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                                                                  Align seg 1/1 to: US-09-724-315-3
                                                                                                                                                                   Ratio: 1.000
Percent Similarity: 100.000
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ARRINGTON, JOSHUA
TITLE OF INVENTION: NUCLEIC ACID ADJUVANTS
FILE REFERENCE: APF41
                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/724,315
CURRENT FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HAYNES, Joel R. APPLICANT: ARRINGTON, JOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/425-8405
TELEFAX: 703/425-8406
INFORMATION FOR SEQ ID NO: 2:
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29 GluTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAl 45
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LENGTH: 2022 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: unknown
MOLECTLE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: McG-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/08582 FILING DATE: 16-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
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1.000
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Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                        Gaps:
Percent Identity:
                                                                  from: 1
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seq_name: /cgn2_6/ptodata/2/pna/US086_COMB.seq:US-08-670-974-6
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SEQ ID NO 1
LENGTH: 5500
TYPE: DNA
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/724,315
CURRENT FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HAYNES, Joel R.
APPLICANT: ARRINGTON, JOSHUA
TITLE OF INVENTION: NUCLEIC ACID ADJUVANTS
FILE REFERENCE: APF41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4109 AAGAGGAACTCAGACGGGATTTGTTAGG 4136
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                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 26-JUN-19
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mekalanos, John J.
APPLICANT: Waldor, Matthew K.
TITLE OF INVENTION: NOVEL CHOLERA VECTORS, VACCINES,
TITLE OF INVENTION: AND METHODS FOR ANTIGEN DELIVERY IN GRAM-NEGATIVE
                  PRIOR APPLICATION DATA:
                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 aArgGlyThrGlnThrGlyPheValArg 54
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                                                                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Wir
                                                                                                                                                                                                                                                                           STREET: 176 P
                                                                                                                                                                                                                                                             STATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                        ZIP: 02110
                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                    176 Federal Street
                                                                                                                                                                                                                                          USA
                                                                                                                    SYSTEM: DOS
FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                         Clark & Elbing LLP
                                                                                                                                                                              Diskette
                                                        UMBER: US/08/670,974
26-JUN-1996
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alignment_scores:
Quality:
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US-09-528-682-1 x US-08-670-974-6
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Quality:
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                                                                                            PCT-US01-16904-1
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                NAME/KEY: misc_feature
LOCATION: (6184). (6184)
OTHER INFORMATION: n can be any one of a, c, g,
NAME/KEY: misc_feature
LOCATION: (6226). (7053)
OTHER INFORMATION: n can be any one of a, c, g,
NAME/KEY: misc_feature
LOCATION: (6224). (6224)
OTHER INFORMATION: n can be any one of a, c, g,
NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: PCT/US01/16904
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,994
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEO ID NOS: 1
SOFTWARE: Patentin version 3.0
SEO ID NO 1
LENGTH: 7586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application PC/TUS0116904 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Methods for Introducing and TITLE OF INVENTION: Bacterial Blebs for Use in FILE REFERENCE: 4115-121 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 6943 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: University of Maryland Biotechnology Institute APPLICANT: Powell, Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5829 GAGTACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCATGC 5878
                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Cholera Toxin Al
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 GluTyrPheAspArgGlyThrGlnMetAsnIleAsnLeuTyrAspHisAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGAGGAACTCAGACGGGATTTGTTAGG 5906
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      26.00
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Percent Identity:
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; LOCATION: (1)..(45)
US-09-040-990-1
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; Sequence 1, Application US/09040990
; GENERAL INFORMATION:
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US-09-528-682-1 x PCT-US01-16904-1
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US-09-528-682-1 x US-09-040-990-1
                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-365-530-1
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Percent Similarity: 100.000
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CURRENT APPLICATION NUMBER: US/09/040,990
CURRENT FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09365530 GENERAL INFORMATION:
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APPLICANT: Friede, M.

TITLE OF INVENTION: USE OF MUTANT ENTEROTOXIN WITH EXCESS B-SUBUNIT AS
TITLE OF INVENTION: ADJUVANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Escherichia coli FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 45
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                APPLICANT: Clements, John D.
APPLICANT: Dickinson, Bonny L.
TITLE OF INVENTION: MUTANT ENTEROTOXIN EFFECTIVE
TITLE OF INVENTION: MON-TOXIC ORAL ADJUVANT
NUMBER OF SEQUENCES: 5
                                                                                                                                                                  NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 GlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 AAGAGGAACTCAGACGGGATTTGTTAGG 164
                                         CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 aArgGlyThrGlnThrGlyPheValArg 54
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGTTGTGGAAATTCATCAAGAACAATTACAGGTGATACTTGTAAT 45
                                                                                                                                 STREET:
                                                                                                                                                  ADDRESSEE:
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                                                                                                                               E: PENNIE & EDMONDS LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.00
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Percent Identity:
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Percent Identity:
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OPERATING SYSTEM:

IBM PC compatible

PC-DOS/MS-DOS

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alignment_block:
US-09-528-682-1 x PCT-US99-30747-8
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US-09-528-682-1 x US-09-365-530-1
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; MOLECULE TYPE:
US-09-365-530-1
                                                                                                                                   alignment_scores:
                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide; OTHER INFORMATION: used to assemble LT-A gene for expression in ; OTHER INFORMATION: plants.

PCT-US99-30747-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:PCT-US99-30747-8
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Ratio: 1.000
Percent Similarity: 100.000
                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-09-365-530-1 from: 1
                                                                                                                                                                                                                                                                                                                         APPLICANT: Boyce Thompson Institute for Plant Research at Cor TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILLING DATE: 199-12-22
NUMBER OF SED ID NOS: 67
SOFTMARE: Patentin Ver. 2.1
SEO ID NO 8
LENGTH: 40
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application PC/TUS9930747
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                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/29
APPLICATION NUMBER: 08/29
APPLICATION DATE: 26-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5113-046
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 GlyCysGlyAsnSerSerArgThrIleThrGlyAspThrCysAsn 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 26-AUG-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212, TELEFAX: 66141 PENNIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                              Quality:
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                                                                                        Ratio:
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Gaps:
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alignment_scores:
                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide; OTHER INFORMATION: used to assemble LT-A gene for expression in COTHER INFORMATION: plants.

PCT-US99-30747-11
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    Sequence 11, Applicati
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PCT-US99-30747-9
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; Sequence 9, Application PC/TUS9930747
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Ratio: 1.000
Percent Similarity: 100.000
Quality: 13.00
Ratio: 1.000
Percent Similarity: 100.000
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APPLICANT: Boyce Thompson Institute for Plant Research at Cor
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 40
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APPLICANT: Boyce Thompson Institute for Plant Research at Cor
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins
TITLE OF INVENTION: Transgenic Plants
TILE REFERENCE: 4868/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEO ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
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Gaps:
Percent Identity:
     Percent Identity:
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alignment_block: US-09-528-682-1 x PCT-US99-30747-12
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Quality:
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US-09-528-682-1 x PCT-US99-30747-11
OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide; OTHER INFORMATION: used to assemble LT-A gene for expression in COTHER INFORMATION: plants.

PCT-US99-30747-14
                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
    Sequence 14, Application PC/TUS9930747
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Ratio: 1.000
Percent Similarity: 100.000
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GENERAL INFORMATION:

APPLICANT: Boyce Thompson Institute for Plant Research at Cor
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins!

TITLE OF INVENTION: Transgenic Plants

FILE REFERENCE: 466,8427

CURRENT APPLICATION NUMBER: PCT/US99/30747

CURRENT FILING DATE: 1999-12-22

NUMBER OF SEQ ID NOS: 67

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 12

LENGTH: 40

TYPE: NAM
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                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                          APPLICANT: BOYGE Thompson Institute for Plant Research at CorTITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed In TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427
CURRENT FILLOATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 67
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                                                                                                                      ORGANISM: Artificial Sequence
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Percent Similarity: 100.000
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TYPE: DNA
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                                              ORGANISM: Artificial Sequence
                                                                          TYPE: DNA
                       FEATURE:
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alignment_scores:

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seq_documentation_block:
Sequence 15, Application PC/TUS9930747
GENERAL INFORMATION:
APPLICANT: Boyce Thompson Institute for Plant Research at CorTITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT APPLICATION NUMBER: PCT/US99/30747
SOURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
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US-09-528-682-1 x PCT-US99-30747-15
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; OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide; OTHER INFORMATION: used to assemble LT-A gene for expression in COTHER INFORMATION: plants.

PCT-US99-30747-17
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                                                                                                                                                                                                 Sequence 17, Application PC/TUS9930747

GENERAL INFORMATION:
APPLICANT: Boyce Thompson Institute for Plant Research at CorTITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILIG DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 67
SOCTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 40
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Percent Identity:
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Percent Identity:
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alignment_block:
US-09-528-682-1 x PCT-US99-30747-17
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PCT-US99-30747-18
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FILE REFERENCE: 4868/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
                                                                                                                       APPLICANT: Boyce Thompson Institute for Plant Research at CorTITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
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                                                                               LENGTH: 40
TYPE: DNA
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TYPE: DNA
OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
                             FEATURE:
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                                                  ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: Boyce Thompson Institute for Plant Research at CorTITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
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Ratio: 1.000
Percent Similarity: 100.000
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APPLICANT: Boyce Thompson Institute for Plant Research at CorTITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 40
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Sequence 30, Application PC/TUS9930747

GENERAL INFORMATION:
APPLICANT: Boyce Thompson Institute for Plant Research at Cor
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 67
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 40
TYPE: DNA
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US-09-528-682-1 x PCT-US99-30747-28/rev
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   Sequence 31, Application PC/TUS9930747
   GENERAL INFORMATION:
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US-09-528-682-1 x PCT-US99-30747-30/rev
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PCT-US99-30747-28
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PCT-US99-30747-30
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Ratio: 1.000
Percent Similarity: 100.000
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Ratio: 1.000
Percent Similarity: 100.000
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           APPLICANT: Boyce Thompson Institute for Plant Research at Cor INVENTION: Orally Immunogenic Bacterial Enterotoxins Title OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn Ver. 2.1
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Gaps:
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US-09-528-682-1 x PCT-US99-30747-33/rev
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PCT-US99-30747-31
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Percent Similarity: 100.000
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Ratio: 1.000
Percent Similarity: 100.000
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Sequence 34, Application PC/TUS9930747

GENERAL INFORMATION:

APPLICANT: BOYGE Thompson Institute for Plant Research at Cor
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/8427

CURRENT APPLICATION NUMBER: PCT/US99/30747
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FILE REFERENCE: 4868/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 199-12-22
NUMBER OF SEO ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEO ID NO 33
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seq_documentation_block:
    Sequence 37, Application PC/TUS9930747
    GENERAL INFORMATION:
    APPLICANT: Boyce Thompson Institute for APPLICANT: Boyce Thompson Institute for INVENTION: Orally Immunogenia
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US-09-528-682-1 x PCT-US99-30747-34/rev
                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:PCT-US99-30747-37
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PCT-US99-30747-34
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APPLICANT: Boyce Thompson Institute for Plant Research at Cor
APPLICANT: Boyce Thompson Institute for Plant Research at Cor
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 67
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 36
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Ratio: 1.000
Percent Similarity: 100.000
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NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 34
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CANT: Boyce Thompson Institute for Plant Research at Cor OF INVENTION: Orally Immunogenic Bacterial Enterotoxins
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seq_documentation_block:
; Sequence 40, Application PC/TUS9930747
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US-09-528-682-1 x PCT-US99-30747-39/rev
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PCT-US99-30747-37
                                                                          seq_name: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:PCT-US99-30747-40
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US-09-528-682-1 x PCT-US99-30747-37/rev
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Ratio: 1.000
Percent Similarity: 100.000
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Ratio: 1.000
Percent Similarity: 100.000
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GENERAL INFORMATION:
APPLICANT: Boyce Thompson Institute for Plant Research at Cor
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427

CURRENT APPLICATION NUMBER: PCT/US99/30747

CURRENT FILING DATE: 1999-12-22

NUMBER OF SEQ ID NOS: 67

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 39
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FILE REFERENCE: 4868/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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Query: US-09-528-682-1
Query length: 240
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Database sequences: 1014543
Database length: 727792371
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-NORM-ext -HEAPSIZE=500 -MINLEN-0 -MASIEN-20000000
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-USER-US09528682_@CGN1_1_476 -NCPU=6 -ICPU=3 -LONGLOG
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Quality:
Ratio:
                                         alignment_block:
US-09-528-682-1 x US-09-809-033A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-140-806-409
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Align seg 1/1
                                                                                                           Quality: 26.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-142-766-409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
ATTORREY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: MCG-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/425-8405
TELEPHONE: 703/425-8406
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09809033A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /ptodata/1/pna/US10_NEW_COMB
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MEDLUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: PATENTIAL PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
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ADDRESSEE: Hendricks and Assoc
STREET: P.O. Box 2509
                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto, Shingo
TITLE OF INVENTION: Chimeric Nontoxic Mutants of
                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                            ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: McGhee, Jerry
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2022 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: 22031
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to: US-09-809-033A-1 from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohmura, Mari
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                                                                                                             Percent
                                                                                                           Length: 26
Gaps: 0
Identity: 100.000
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1.4e+03
1.4e+03
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L.4e+03
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L.4e+03
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; ANTI-SENSE: NO ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-809-033A-2
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                                                                            Align seg 1/1
                                                                                                                     US-09-528-682-1 x US-09-809-033A-2
                                                                                                                                                                                 Ratio: 1.000
Percent Similarity: 100.000
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TELEPHONE: 703/425-8405
TELEFAX: 703/425-8406
INFORMATION FOR SEQ ID NO: 2:
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656 GAGTACTTTGACCGAGGTACTCAAATGAATATCAACCTTTATGATCATGC 705
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                   ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2022 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/809,033A
FILING DAYE: 16-Mar-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hendaricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: McG-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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ADDRESSEE: Hendricks and Assoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Chimeric Nontoxic Mutants of Enterotoxins as Mucosal Adjuvants for Cell-Mediated
                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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                                                                            to: US-09-809-033A-2
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Takeda, Yoshifumi
Ohmura, Mari
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alignment_block:
US-09-528-682-1 x US-10-105-299-12399/rev
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; Sequence 12399, Application
               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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Quality:
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; ORGANISM: Homo sapiens
US-10-105-299-12399
                                                                                    ; ORGANISM: Human
US-10-027-632-242566
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
Prior Application removed - See File Wrapp SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12399
LENGTH: 406
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                                                                                                                                                                                SEQ ID NO 242566
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TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILLING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                            SOFTWARE: FastSEQ
                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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Gaps: 0
Percent Identity: 100.000
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                                                                                                   seq_documentation_block:
; Sequence 203067, Appli
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US-09-528-682-1 x US-10-027-632-67507/rev
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Quality:
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, NAME/KEY: misc_feature

; LOCATION: (1)...(651)

; OTHER INFORMATION: n = A,T,C

US-10-027-632-67507
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                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-203067
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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Percent Similarity:
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                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 67507
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APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 651
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                                                                                                                                                                                                                              390 TCCACCTCTCTGAGCCTCAGATCC 367
                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                            SerThrSerLeuSerLeuArgSer 68
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                                                                                                      Application US/10027632
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Gaps:
Percent Identity:
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Gaps: 0
Percent Identity: 100.000
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6 651

CURRENT APPLICATION NUMBER: US/10/027,632

REFERENCE: 108827.129

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alignment_block:
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Percent Similarity: 100.000
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LENGTH: 672
                                                                                                                SEQ ID NO 8851
LENGTH: 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-08-09
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/146,002
NAME/KEY: misc_feature
                                                     ORGANISM: Human
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1.000
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alignment_scores: 8.00 Quality: 8.00 Ratio: 1.000 Percent Similarity: 100.000
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; OTHER INFORMATION: n = A,T,C or
US-10-027-632-8851
                                                                                                                                                                                       alignment_block:
US-09-528-682-1 x US-10-027-632-8852/rev
seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-125010
                                                                                                                                                                                                                                                                                                             alignment_scores:
    Quality:
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Ratio: 1.000
Percent Similarity: 100.000
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APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FASTSEQ
SEQ ID NO 8852
LENGTH: 797
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR FILING DATE: 1999-11-23 PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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LOCATION: (1)...(797)
OTHER INFORMATION: n = A,T,C
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                 277 AGTGCCCATCTGGCTGGCCAGAGC 254
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                                                                                             68 SerAlaHisLeuAlaGlyGlnSer 75
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Percent Identity:
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alignment_block:
US-09-528-682-1 x US-10-027-632-125010
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Quality:
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; ORGANISM: Human
US-10-027-632-125010
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; Sequence 125010, Applicati
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
                                                                     CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/165,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
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Ratio: 1.000
Percent Similarity: 100.000
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SEQ ID NO 125010
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR EILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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PRIOR APPLICATION NUMBER: US 60/146,002
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                                                   PRIOR FILING DATE: 1999-08-09
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for Windows Version 4.0
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Gaps: 0
Percent Identity: 100.000
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; LENGTH: 970
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-323968
seq_documentation_block:
; Sequence 258165, Application US/10027632
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US-09-528-682-1 x US-10-027-632-258164/rev
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US-09-528-682-1 x US-10-027-632-323968
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Ratio: 1.000
Percent Similarity: 100.000
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LENGTH: 970
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SEQ ID NO 258164
LENGTH: 2211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                TACAGGAATCTGAATATTGCTCCG 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/146,002 FILING DATE: 1999-08-09
                                                                  /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-258165
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Gaps:
Percent Identity:
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Percent Identity:
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alignment_block:
US-09-528-682-1 x US-10-027-632-258165/rev
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; ORGANISM: Human
US-10-027-632-258165
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Sequence 112146, Application US/10027632
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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SEQ ID NO 258165
LENGTH: 2211
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                               NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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            Q ID NO 112146
LENGTH: 2732
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Gaps: 0
Percent Identity: 100.000
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Gaps:
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to:
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                                 seq_documentation_block:
; Sequence 53058, Applica
; GENERAL INFORMATION:
; APPLICANT: Wang, Davio
CANT: Wang, David G. OF INVENTION: Identification and Mapping of Single Nucleotide
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alignment_block:
US-09-528-682-1 x US-10-138-381-26/rev
                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Vibrio cholerae
US-10-138-381-26
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    Quality:
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seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-53058
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Ratio: 1.000
Percent Similarity: 100.000
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LENGTH: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 08/968,046
PRIOR FILLING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 08/328,710
PRIOR FILLING DATE: 1994-10-25
PRIOR APPLICATION NUMBER: 6-48174 JAPAN
PRIOR FILLING DATE: 1994-03-18
PRIOR APPLICATION NUMBER: 6-30277 JAPAN
PRIOR APPLICATION NUMBER: 6-30277 JAPAN
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CURRENT APPLICATION NUMBER: US/10/138,381
CURRENT FILING DATE: 2002-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OHASHI, Tetsuo
TITLE OF INVENTION: Oligonucleotides for Detecting Bacteria and
TITLE OF INVENTION: Detection Process
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1994-02-28
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                                           162 TyrArgLeuAlaGlyPheProPro 169
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Gaps: 0
Percent Identity: 100.000
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Percent Identity:
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Application US/10027632

FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30

Polymorphisms in the

Human Genome

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; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00919904
US-09-539-331D-20665
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                                                                   alignment_scores:
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PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
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Ratio: 1.000
Percent Similarity: 100.000
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SOFTWARE: FastSEQ for
SEQ ID NO 53058
                                                                                                                                                                                                                                                SOFTWARE: PERL Program.
SEQ ID NO 20665
LENGTH: 102
TYPE: DNA
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CURRENT APPLICATION NUMBER: US/09/539,331D
CURRENT FILING DATE: 2000-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mullahy, Sara J.

APPLICANT: Naughton, Rebecca E.

TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                        Prior Application removed – See File Wrapper or Palm NUMBER OF SEQ ID NOS: 40961
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Ratio:
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  Percent Identity:
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                    Length:
Gaps:
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APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(1530)B
CURRENT APPLICATION NUMBER: US/09/975,254
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US/09/263,191
PRIOR APPLICATION NUMBER: US/09/263,191
PRIOR APPLICATION STEE 1999-03-05
SEQ ID NO 14267
LENGTH: 158
TYPE: DNA
ORGANISM: Glycine max
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 700908892H1
US-09-975-254-14267
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us-09-528-682-1 x us-09-539-331D-20665/rev
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; Sequence 266, Application US/09673476
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US-09-528-682-1 x US-09-975-254-14267
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NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver.
SEQ ID NO 266
LENGTH: 217
TYPE: DNA
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                 APPLICANT: BILLAULT, ALAIN

ITTLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
TITLE OF INVENTION: MYCOBACTERIA.
FILE REFERENCE: 05394.0011-00000
CURRENT APPLICATION NUMBER: US/09/673,476
CURRENT FILING DATE: 2002-03-29
CURRENT FILING DATE: 2002-03-29
                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/IB99/00740 PRIOR FILING DATE: 1999-04-16
                                                                                                                                  PRIOR FILING DATE: 1998-04-16
                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/060,756
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Gaps:
Percent Identity:
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                     NUMBER OF SEQ ID NOS: 1
SOFTWARE: PERL Program
SEQ ID NO 8128
LENGTH: 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/539,800C CURRENT FILING DATE: 2000-03-30 PRIOR APPLICATION NUMBER: 08/21,383 PRIOR FILING DATE: August 16, 1995 PRIOR APPLICATION NUMBER: 08/271,217 PRIOR APPLICATION NUMBER: 08/334,881 PRIOR APPLICATION NUMBER: 08/334,881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: November 4, 1994
PRIOR APPLICATION NUMBER: 08/943,978
PRIOR FILING DATE: October 3, 1997
PRIOR APPLICATION NUMBER: 60/028,732
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR
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TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE
FILE REFERENCE: PD-1023 CIP
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PRIOR APPLICATION NUMBER: 60/111
                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: February 12, 1 PRIOR APPLICATION NUMBER: 09/452,
                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/250,003
                                                                                                                                                                                                                              PRIOR FILING DATE: December
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER:
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                     OTHER INFORMATION: Incyte ID No: hu00121720
                                                                                      ORGANISM: Homo sapiens
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                                          NAME/KEY: misc_feature
                                                                        FEATURE:
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APPLICATION NUMBER: 08/943,
FILING DATE: October 4, 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/993,
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/034,975
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Delegeane, Angelo M.
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Stuve, Laura L.
                                                                                                                                                                                                                                                                                                                                           February 10, 1999
NUMBER: 60/074,364
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Gaps: 0
Percent Identity: 100.000
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APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15309)8
COURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US/09/263,191
PRIOR APPLICATION NUMBER: US/09/263,191
PRIOR APPLICATION NUMBER: US/09/263,191
PRIOR FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 31255
SEQ ID NO 23834
LENGTH: 234
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 700962842H1
US-09-975-254-23834
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US-09-528-682-1 x US-09-539-800C-8128
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; LOCATION: 60, 178
; OTHER INFORMATION:
US-09-539-800C-8128
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; Sequence 13594, Application US/09539331D
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Ratio: 1.000
Percent Similarity: 100.000
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APPLICANT:
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                                     APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
FILE REFERENCE: PD-1022 CIP
CURRENT APPLICATION NUMBER: US/09/539,331D CURRENT FILING DATE: 2000-03-30
                                                                                                             APPLICANT:
                                                                                                                              APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: DeLegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuye, Laura L.
                                                                                                                                                                                                                                                                                                                                                                173 TCTCTAAGCCTACGGTCTGCT 153
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                                                                                                           Mullahy, Sara J.
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Percent Identity:
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alignment_scores: 7.00
Quality: 7.00
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 08/972,899
PRIOR FILING DATE: November 18, 1997
PRIOR APPLICATION NUMBER: 08/395,244
PRIOR APPLICATION NUMBER: 07, 1995
PRIOR APPLICATION NUMBER: 08/722,922
PRIOR FILING DATE: September 27, 1996
PRIOR APPLICATION NUMBER: 60/005,526
PRIOR APPLICATION NUMBER: 60/005,526
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NUMBER OF SEQ ID NOS: 40961
SOFTWARE: PERL Program
SEQ ID NO 13594
LENGTH: 239
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TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
FILE REFERENCE: PD-1037 CIP
CURRENT APPLICATION NUMBER: US/09/540,210B
CURRENT FILING DATE: 2002-04-03.
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OTHER_INFORMATION: Incyte ID No: hu00527775
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OR APPLICATION NUMBER: 08/824,029
OR FILING DATE: March 25, 1997
OR APPLICATION NUMBER: 60/014,010
FOR FILING DATE: March 25, 1996
OR APPLICATION NUMBER: 08/826,847
OR FILING DATE: April 10, 1997
OR FILING DATE: April 10, 1996
OR FILING DATE: April 10, 1996
OR APPLICATION NUMBER: 08/903,555
OR APPLICATION NUMBER: 08/903,555
OR FILING DATE: July 31, 1997
OR FILING DATE: July 31, 1996
OR FILING DATE: July 31, 1996
OR FILING DATE: July 31, 1996
OR FILING DATE: July 31, 1997
OR APPLICATION NUMBER: 60/023,308
OR APPLICATION NUMBER: 60/023,308
OR APPLICATION NUMBER: 08/862,178
OR FILING DATE: May 22, 1997
OR APPLICATION NUMBER: 60/018,217
OR APPLICATION NUMBER: 60/018,217
OR APPLICATION NUMBER: 60/881,589
OR FILING DATE: May 23, 1996
OR APPLICATION NUMBER: 08/881,589
OR FILING DATE: June 24, 1997
OR FILING DATE: June 24, 1997
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Delegeane, Angelo M.
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Stuve, Laura L.
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Gaps:
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PRIOR APPLICATION NUMBER: 50/049,975;
PRIOR FILING DATE: June 9, 1998;
PRIOR FILING DATE: June 13, 1997;
NUMBER OF SEQ ID NOS: 35654;
SOFTWARE: PERL Program
SEQ ID NO 11353;
LENGTH: 242;
TYPF: P. 242
FEATURE:

NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID NO
NAME/KEY: unsure
LOCATION: 7, 93, 186, 204
OTHER INFORMATION: a, t, c, g,
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                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/107,592
FILING DATE: June 30, 1998
APPLICATION NUMBER: 60/052,751
FILING DATE: July 1, 1997
APPLICATION NUMBER: 09/094,079
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/
FILING DATE: May 29, 19
FILING DATE: May 29, 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: February 13, 1997
APPLICATION NUMBER: 09/035,172
FILING DATE: March 4, 1998
APPLICATION NUMBER: 60/040,431
FILING DATE: March 5, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/015,533
FILING DATE: April 10, 1996
APPLICATION NUMBER: 08/755,524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/025,217
FILING DATE: August 22, 1996
APPLICATION NUMBER: 08/937,142
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                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/074,999 FILING DATE: May 8, 1998
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60 FILING DATE: April 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09 FILING DATE: March 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60 FILING DATE: March 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/041,894 FILING DATE: March 12, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/826,847 FILING DATE: April 10, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/903,471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N NUMBER: 08/96
E: October 29,
N NUMBER: 60/03
E: October 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER: 60/039,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER: 09/021,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : September 23, 1997
NUMBER: 60/026,598
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July 31, 1997
NITMBER: 60/023,308
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ER: 08/903,802
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R: 60/048,431
29, 1997
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L, 1997
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L1, 1997
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l4, 1997
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No: hu00067358

or other

US-09-540-210B-11353

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seq_documentation_block:
; Sequence 8235, Application US/09539800C
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-528-682-1 x US-09-539-331D-9255/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-528-682-1 x US-09-540-210B-11353
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Quality:
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; OTHER INFORMATION: Incyte ID No: hu00523285
US-09-539-331D-9255
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                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-539-800C-8235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
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SEQ ID NO 9255
LENGTH: 253
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APPLICANT:
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                                                                                                  APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuye, Laura L.
                   TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE FILE REFERENCE: PD-1023 CIP
                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 40961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/539,331D CURRENT FILING DATE: 2000-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Stuve, Laura L. APPLICANT: Mullahy, Sara J.
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CURRENT APPLICATION NUMBER: US/09/539,800C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE FILE REFERENCE: PD-1022 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 LysValLysArgGlnIlePhe 223
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Stuve, Laura L.
                                                              Naughton, Rebecca E.
                                                                             Mullahy, Sara J
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alignment_block:
US-09-528-682-1 x US-09-539-800C-8235/rev
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; Sequence 15360, Application US/09540210B
; GENERAL INFORMATION:
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; OTHER INFORMATION: Incyte ID No: hu00266046
US-09-539-800C-8235
                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-540-210B-15360
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Ratio: 1.000
Percent Similarity: 100.000
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SOFTWARE: PERL Program
SEQ ID NO 8235
LENGTH: 272
                                                            APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Maughton, Rebecca E.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
FILE REFERENCE: PD-1037 CIP
CURRENT APPLICATION NUMBER: US/09/540,210B
CURRENT FILING DATE: 2007-04-03
PRIOR APPLICATION NUMBER: 08/972,899
PRIOR FILING DATE: NOVember 18, 1997
PRIOR FILING DATE: NOVember 18, 1997
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PRIOR APPLICATION NUMBER: 08/395,244 PRIOR FILING DATE: February 27, 1995 PRIOR APPLICATION NUMBER: 08/722,922
                                                                                                                                                                                                                                                                                  APPLICANT: Seilhamer, Jeffrey J. APPLICANT: Delegeane, Angelo M.
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PRIOR APPLICATION NUMBER: 08/334,881
PRIOR FILING DATE: November 4, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: August 16, 1995
PRIOR APPLICATION NUMBER: 08/271,217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 AGGGCTGATTCTCGGCCCCCC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 ArgAlaAspSerArgProPro 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/111,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: February
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: October 4, 1997 APPLICATION NUMBER: 60/027,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/943,979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/452,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: October
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               December
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity:
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6
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September 27, 1996 WUMBER: 60/005,526

September

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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No:
US-09-540-210B-15360
                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/540,210B
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 08/972,899
PRIOR FILING DATE: November 18, 1997
PRIOR APPLICATION NUMBER: 08/395,244
PRIOR APPLICATION NUMBER: 08/395,244
PRIOR FILING DATE: February 27, 1995
PRIOR APPLICATION NUMBER: 08/722,922
PRIOR FILING DATE: September 27, 1996
PRIOR APPLICATION NUMBER: 60/005,526
PRIOR APPLICATION NUMBER: 08/824,029
PRIOR FILING DATE: March 25, 1997
PRIOR APPLICATION NUMBER: 60/014,010
PRIOR APPLICATION NUMBER: 60/014,010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-540-210B-20652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/048,431
PRIOR FILING DATE: May 29, 1997
PRIOR PELICATION NUMBER: 09/107,592
PRIOR FILING DATE: June 30, 1998
PRIOR APPLICATION NUMBER: 60/052,751
PRIOR FILING DATE: June 30, 1997
PRIOR APPLICATION NUMBER: 09/094,079
PRIOR APPLICATION NUMBER: 09/094,079
PRIOR APPLICATION NUMBER: 09/094,975
PRIOR APPLICATION NUMBER: 60/044,975
PRIOR APPLICATION NUMBER: 60/044,975
PRIOR FILING DATE: June 13, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-528-682-1 x US-09-540-210B-15360/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20652, Application US/09540210B
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 15360
LENGTH: 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 35654
SOFTWARE: PERL Program
SEQ ID NO 15360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mullahy, Sara J.

APPLICANT: Naughton, Rebecca E.

TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE FILE REFERENCE: PD-1037 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 ThrSerLeuSerLeuArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 ACCAGCCTCTCCCTGAGGAGC
                                                                                                      APPLICATION NUMBER: 08/
FILING DATE: APT11 10,
APPLICATION NUMBER: 60/
FILING DATE: APT11 10,
                                                                                                                                                                                            FILING DATE: March 25, APPLICATION NUMBER: 60, FILING DATE: March 25,
                                            APPLICATION NUMBER:
                                                                                        APPLICATION NUMBER:
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Stuve, Laura
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: July 31, 1
NUMBER: 08,
                                                              July 31,
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                                                                                                                                                     25, 1996
: 08/826,847
10, 1997
                                                                 08/903,555
11, 1997
                                                                                                           60/015,533
10, 1996
                       60/023,308
L, 1996
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Percent Identity:
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OR APPLICATION NUMBER: 08/903,556
OR FILING DATE: July 31, 1997
OR APPLICATION NUMBER: 60/025,217
OR FILING DATE: August 22, 1996
OR APPLICATION NUMBER: 08/937,142
OR FILING DATE: September 23, 1997
OR APPLICATION NUMBER: 08/937,142
OR FILING DATE: September 24, 1996
OR APPLICATION NUMBER: 08/07,746
OR FILING DATE: October 29, 1997
OR APPLICATION NUMBER: 00/030,144
OR FILING DATE: October 30, 1996
OR APPLICATION NUMBER: 60/030,144
OR FILING DATE: APPLI 10, 1997
OR APPLICATION NUMBER: 60/035,533
OR FILING DATE: APPLI 10, 1996
OR APPLICATION NUMBER: 08/755,524
OR APPLICATION NUMBER: 08/0707,495
OR APPLICATION NUMBER: 08/0707,495
OR FILING DATE: November 22, 1995
OR APPLICATION NUMBER: 09/007,495
OR APPLICATION NUMBER: 09/007,495
OR FILING DATE: November 22, 1995
OR APPLICATION NUMBER: 09/007,495
OR APPLICATION NUMBER: 09/007,495
OR FILING DATE: November 22, 1995
OR APPLICATION NUMBER: 09/007,495
OR APPLICATION NUMBER: 09/007,495

R APPLICATION N R FILING DATE: R APPLICATION N R FILING DATE: R APPLICATION N

NE February 13, 1997
NE NUMBER: 09/035,172
E: March 4, 1998
NN NUMBER: 60/040,431
NE March 12, 1997
NN NUMBER: 09/041,894
E: March 12, 1998
RE: March 14, 1997
NN NUMBER: 09/050,817
E: March 30, 1998
NN NUMBER: 60/043,792
E: March 11, 1997
NN NUMBER: 09/074,999

FILING DATE:

FILING

APPLICATION N
FILING DATE: APPLICATION FILING DATE:

: February 1

/039,

APPLICATE: June R FILING DATE: June R FILING DATE: July 31, 1997
PTLING DATE: July 31, 1997
PTLING DATE: JULY 31, 1996
PTLING DATE: 31, 1996
PTLING DATE: JUNE R. 10,705, 881

NUMBER: 60/021,275

OR FILING DATE: July 31, 1996
NR APPLICATION NUMBER: 08/905,881
OR APPLICATION NUMBER: 10,1997
OR APPLICATION NUMBER: 60/025,204
OR FILING DATE: August 1, 1996
OR APPLICATION NUMBER: 08/903,471
OR APPLICATION NUMBER: 08/903,471
OR APPLICATION NUMBER: 60/025,478
OR APPLICATION NUMBER: 60/025,478
OR APPLICATION NUMBER: 60/025,478

NUMBER: 08/903,556
NUMBER: 08/903,556

OR APPLICATION NUMBER: 08/824,029
OR FILING DATE: MATCh 25,1997
OR APPLICATION NUMBER: 60/014,010
OR FILING DATE: MATCh 25,1996
OR APPLICATION NUMBER: 08/826,847
OR FILING DATE: APT11 10,1997
OR APPLICATION NUMBER: 60/015,533
OR FILING DATE: APT11 10,1996
OR APPLICATION NUMBER: 08/903,555
OR FILING DATE: July 31,1996
OR APPLICATION NUMBER: 60/023,308
OR FILING DATE: July 31,1996
OR APPLICATION NUMBER: 08/862,178
OR FILING DATE: May 22, 1997
OR APPLICATION NUMBER: 60/018,217
OR APPLICATION NUMBER: 60/018,217
OR APPLICATION NUMBER: 60/08,217
OR APPLICATION NUMBER: 60/018,217
OR APPLICATION NUMBER: 60/08,881,589
OR APPLICATION NUMBER: 60/881,589
OR APPLICATION NUMBER: 08/881,589
OR APPLICATION NUMBER: 08/881,589
OR APPLICATION NUMBER: 08/881,589

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SOFTWARE: PERL Program
SEQ ID NO 20652
LENGTH: 282
TYPE: DNA
                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/052,751
PRIOR FILLNG DATE: July 1, 1997
PRIOR APPLICATION NUMBER: 09/094,079
PRIOR FILLNG DATE: June 9, 1998
PRIOR APPLICATION NUMBER: 60/049,975
PRIOR FILING DATE: June 13, 1997
                                                                                                                                                  NUMBER OF SEQ ID NOS: 35654
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COR FILING DATE: February 13, 1997
OR APPLICATION NUMBER: 09/035,172
OR FILING DATE: MARICH 4, 1998
OR FILING DATE: MARICH 5, 1997
OR APPLICATION NUMBER: 09/041,894
OR FILING DATE: MARICH 5, 1997
OR APPLICATION NUMBER: 09/041,894
OR FILING DATE: MARICH 12, 1998
OR APPLICATION NUMBER: 60/040,199
OR FILING DATE: MARICH 14, 1997
OR FILING DATE: MARICH 14, 1997
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OR APPLICATION NUMBER: 60/026,598
OR FILING DATE: September 24, 1996
OR APPLICATION NUMBER: 08/960,746
OR FILING DATE: October 29, 1997
OR APPLICATION NUMBER: 60/030,144
OR FILING DATE: October 30, 1996
OR APPLICATION NUMBER: 60/015,533
OR FILING DATE: April 10, 1997
OR APPLICATION NUMBER: 60/015,533
OR FILING DATE: April 10, 1996
OR APPLICATION NUMBER: 08/755,524
OR APPLICATION NUMBER: 08/755,524
OR FILING DATE: November 22, 1995
OR APPLICATION NUMBER: 60/007,495
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RAPPLICATION NUMBER: 08/905,881
DR FILING DATE: August 1, 1997
OR APPLICATION NUMBER: 60/025,204
OR FILING DATE: August 1, 1996
DR APPLICATION NUMBER: 08/903,471
OR FILING DATE: July 30, 1997
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REAPPLICATION NUMBER: 60/025,478
REFLING DATE: July 31, 1996
OR APPLICATION NUMBER: 08/903,556
OR FILING DATE: July 31, 1997
REAPPLICATION NUMBER: 60/025,217
OR FILING DATE: August 22, 1996
OR APPLICATION NUMBER: 608/937,142
OR ESTITING NATE: 608/937,142
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FILING DATE: JULY 31, 1997
RAPPLICATION NUMBER: 60/023, 308
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: May 29, 1997
APPLICATION NUMBER: 09/107,592
FILING DATE: June 30, 1998
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APPLICATION NUMBER: 08/881,589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/074,999 FILING DATE: May 8, 1998 APPLICATION NUMBER: 60/048,431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: March 30, 1998
APPLICATION NUMBER: 60/043,792
FILING DATE: April 11, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/050,817
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Tune 24, 195,
TIMBER: 60/021,275
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; OTHER INFORMATION: Incyte ID No: hu00094015; NAME/KEY: unsure; LOCATION: 189-190, 229; OTHER INFORMATION: a, t, c, g, or other US-09-540-210B-20652
                                                                                   seq_documentation_block:
; Sequence 22417, Application US/09539331D
; GENERAL INFORMATION:
                                                                                                                                                                       seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-539-331D-22417
                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-528-682-1 x US-09-539-331D-28303
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US-09-528-682-1 x US-09-540-210B-20652/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2000-03-30

Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 40961

SOFTWARE: PERL Program
SEQ ID NO 28303

LENCTH: 312

TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: US-09-540-210B-20652
                                                                                                                                                                                                                                                                                                         Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28303, Application US/09539331D
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYUNCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
FILE REFERENCE: DD-1022 CIP
CURRENT APPLICATION NUMBER: US/09/539,331D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Seilhamer, Jeffrey J. APPLICANT: Delegeane, Angelo M.
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00114685
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                                                                                                                                                                                                                    AGCCTGAGTCTGAGGAGTGCA 51
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Stuve, Laura L
                                                                                                                                                                                                                                                                                                         US-09-539-331D-28303
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Gaps:
Percent Identity:
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Gaps: 0
Percent Identity: 100.000
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100.000
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seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-721-544-15587

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APPLICANT: Mullahy, Sara J.

APPLICANT: Naughton, Rebecca E.

TITLE OF INVENTION: POLYNUCLECTIDES OF CARDIOVASCULAR SYSTEM TISSUE FILE REFERENCE: PD-1022 CIP
CURRENT APPLICATION NUMBER: US/09/539,331D
CURRENT ETILING DATE: 2000-03-30
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 40961
SOFTWARE: PERL Program
SEQ ID NO 22417
LENGTH: 318
TYPE: DNA
ORGANTT
                                                                                                                                                                                                                                                                                                  ; NUMBER OF SEQ ID NOS: 2959
; SEQ ID NO 160
; LENGTH: 323
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-USO2-10421-160
                                                                                                               alignment_block:
US-09-528-682-1 x PCT-US02-10421-160
                                                                                                                                                                                                                                         alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:PCT-US02-10421-160
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: LOCATION: 45, 51, 64, 78, 93, 108, 144, 150, 168, 216,
: OTHER INFORMATION: a, t, c, g, or other
US-09-539-331D-22417
                                                                                                                                                                        Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
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Ratio: 1.000
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                                                                             Align seg 1/1 to: PCT-US02-10421-160
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                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 210121.565PC
CURRENT APPLICATION NUMBER: PCT/US02/10421
CURRENT FILING DATE: 2002-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Corixa Corporation APPLICANT: Wang, Tongtong APPLICANT: Wang, Siging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF CANCER
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OTHER INFORMATION: Incyte ID No: hu00325793
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71
                                   63 SerLeuSerLeuArgSerAla 69
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TCTCTTTCTCTCAGAAGTGCT 91
                                                                                                                                                                                                                  Quality:
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Gaiger, Alexander
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seq_documentation_block:
; Sequence 160, Application US/10112699
; GENERAL INFORMATION:
                                                                                                                                         seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-112-699-160
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US-09-528-682-1 x US-09-721-544-15587/rev
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; Sequence 15587, Application US/09721544
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Ratio: 1.000
Percent Similarity: 100.000
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15587
LENGTH: 323
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APPLICANT: Wang, Tongtong
APPLICANT: Wang, Siqing
APPLICANT: Bangur, Chaitanya S.
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CURRENT APPLICATION NUMBER: US/09/721,544
CURRENT FILING DATE: 2000-11-21
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APPLICANT: Yang, Fei
APPLICANT: Yim, Kenneth
TITLE OF INVENTION: NOVel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From a cDNA Library of Fetal Liver-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/515,128 PRIOR FILING DATE: 1998-02-13 PRIOR APPLICATION NUMBER: 09/034,341
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Labat, Ivan
Laroya, wimi
Lomelli, Michelle
Nguyen, Phuong
Nogra, Margie
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Engleman, Carrie
Faulkner, Brandy
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Tran, Lien
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Giedt, Gretchen
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Drake, Jim
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Percent Identity:
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; APPLICANT: Gaiger, Alexander
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; TITLE OF INVENTION: AND DIAGNOSIS OF CANCER
; FILE REFERENCE: 210121.565
; CURRENT APPLICATION NUMBER: US/10/112,699
; CURRENT FILING DATE: 2007-03-28
; NUMBER OF SEQ ID NOS: 2959
; SEQ ID NO 160
; SEQ ID NO 160
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Quality:
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Ratio: 1.000
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Sequence 15776, Applic
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                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 08/521,383
PRIOR FILING DATE: August 16, 1995
PRIOR APPLICATION NUMBER: 08/71,217
PRIOR FILING DATE: June 27, 1994
PRIOR APPLICATION NUMBER: 08/334,881
PRIOR FILING DATE: November 4, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: PD-1023 CIP
CURRENT APPLICATION NUMBER: US/09/539,800C
CURRENT FILING DATE: 2000-03-30
                                PRIOR FILING DATE: Dec
                                                                                      PRIOR FILING DATE: February PRIOR APPLICATION NUMBER: PRIOR FILING DATE: Decembe
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PRIOR APPLICATION NUMBER: 60/028
PRIOR FILING DATE: October 4, 199
PRIOR FILING DATE: October 4, 199
                                                                    PRIOR APPLICATION NUMBER: 60/111
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PRIOR FILING DATE: October 4, 199
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ID NO
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APPLICATION NUMBER: 60/074,364
                                                                                                                                                                                                          APPLICATION NUMBER: 60/034,975
                                                                                                                                                                                                                          APPLICATION NUMBER: 08/993,774 FILING DATE: December 18, 1997
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                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/027
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                  PERL Program
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Stuve, Laura L.
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NUMBER: 09/452,
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FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu01286321
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FILING DATE:
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Naughton, Rebe
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                                                                                                                                                       NUMBER: 60
                  : April 24, 1997
NUMBER: 60/016,
: April 24, 1996
                                                                                                                                                                                                                                                                                                                                              NUMBER: 08/951,197
: October 1, 1997
NUMBER: 60/027,249
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Gaps:
Percent Identity:
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alignment_scores:
Quality:
Ratio:
                                                                                                                                                                    ; NAME/KEY: unsure
; LOCATION: 37, 56, 60,
; OTHER INFORMATION: a,
US-09-539-806B-4227
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PRIOR APPLICATION NUMBER: 60/031,667
PRIOR FILING DATE: NOVember 11, 1996
PRIOR FILING DATE: NOVember: 08/901,902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR EILING DATE: Febbruary 13, 1997
PRIOR APPLICATION NUMBER: 09/045,574
PRIOR APPLICATION NUMBER: 60/041,275
PRIOR FILING DATE: March 20, 1998
PRIOR APPLICATION NUMBER: 60/041,275
PRIOR FILING DATE: March 16, 1997
PRIOR FILING DATE: March 16, 1998
PRIOR APPLICATION NUMBER: 60/043,613
PRIOR FILING DATE: March 18, 1997
PRIOR APPLICATION NUMBER: 09/057,988
PRIOR APPLICATION NUMBER: 09/079,988
PRIOR APPLICATION NUMBER: 09/143,256
PRIOR FILING DATE: APP11 16, 1998
PRIOR APPLICATION NUMBER: 09/114,041
PRIOR APPLICATION NUMBER: 09/114,041
PRIOR APPLICATION NUMBER: 09/114,041
PRIOR APPLICATION NUMBER: 09/124,041
PRIOR APPLICATION NUMBER: 09/124,041
PRIOR APPLICATION NUMBER: 09/125,340
PRIOR APPLICATION NUMBER: 09/145,340
             Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
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SOFTWARE: PERL Program
SEQ ID NO 4227
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PRIOR FILING DATE: September 1: 198
NUMBER OF CO.
                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
OTHER INFORMATION: Incyte
                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                          FEATURE:
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OR APPLICATION NUMBER: 08,918,181
OR FILING DATE: August 27, 1997
OR APPLICATION NUMBER: 60,023,236
OR FILING DATE: August 28, 1996
OR APPLICATION NUMBER: 09,940,864
OR FILING DATE: September 29, 1997
OR APPLICATION NUMBER: 60,027,236
OR FILING DATE: September 30, 1996
OR APPLICATION NUMBER: 08,956,502
OR FILING DATE: October 23, 1997
OR APPLICATION NUMBER: 07,029,083
OR FILING DATE: October 23, 1996
OR APPLICATION NUMBER: 08,993,402
OR FILING DATE: December 18, 1997
OR APPLICATION NUMBER: 60,033,647
OR FILING DATE: December 19, 1996
OR APPLICATION NUMBER: 60,033,647
OR FILING DATE: December 19, 1996
OR APPLICATION NUMBER: 60,033,647
OR FILING DATE: February 11, 1996
OR APPLICATION NUMBER: 60,044,847
OR FILING DATE: February 13, 14,037
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Length: 7
Gaps: 0
Percent Identity: 100.000
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g, or other
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PRIOR APPLICATION NUMBER: 09/034,341
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 24489
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19743
LENGTH: 356
TYPE: DNA
ORGANISM: Homo sapiens
US-09-721-544-19743
                                                                                         alignment_block:
US-09-528-682-1 x US-09-721-544-19743
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US-09-528-682-1 x US-09-539-806B-4227
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Quality:
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APPLICANT: Yim, Kenneth
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From a cDNA Library of Fetal Liver-Sg
FILE REFERENCE: 728CIP
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CURRENT FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 09/515,128
PRIOR FILING DATE: 1998-02-13
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INFORMATION:
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Laroya, Mimi
Lomelli, Michelle
Nguyen, Phuong
Nogra, Margie
Palencia, Servando
Raisi, Fariba
Smith, Benjamin
Tkach, Joe
Tran, Lien
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Faulkner, Brandy
Garcia, Veronica
Giedt, Gretchen
                                                                                                                                                      Ratio:
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Jones, Lee
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Dickson, Mark
Drake, Jim
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                                                            US-09-721-544-19743
                                                                                                                                       Length: 7
Gaps: 0
Percent Identity: 100.000
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alignment_block:
US-09-528-682-1 x US-10-011-154-2094/rev
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Ratio: 1.000
Percent Similarity: 100.000
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SEQ ID NO 2094
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                                                           SEQ ID NO 3305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                               PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/156,358
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                                  ENGTH: 435
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                                                                                     FastSEQ for
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Dickson, Mark C.
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                                                                                     Windows Version 4.0
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Gaps: 0
Percent Identity: 100.000
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; Sequence 89412, Application US/10027632
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US-09-528-682-1 x US-10-011-154-2817
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US-10-011-154-2817
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Ratio: 1.000
Percent Similarity: 100.000
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Ratio: 1.000
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PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/404,284
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 4670
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 2817
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                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                          APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30
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CURRENT FILING DATE: 2001-12-06
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TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                           65 SerLeuArgSerAlaHisLeu 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Labat, Ivan
Stache-Crain, Birgit
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Percent Identity:
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FILING DATE: 2000-04-20

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seq_documentation_block:
Sequence 89413, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108027.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/27,632
CURRENT FILING DATE: 2002-04-20
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,318
PRIOR APPLICATION NUMBER: US 60/187,363
                        alignment_scores:
Quality:
Ratio:
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Quality:
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; ORGANISM: Human
US-10-027-632-89412
                                                                                                                                                         ; ORGANISM: Human US-10-027-632-89413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-89413
Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                  SOFTWARE: FastS
SEQ ID NO 89413
LENGTH: 448
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Percent Similarity: 100.000
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 89912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID
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                                                                                                                                                                                                                                                                                        for Windows Version 4.0
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Gaps: 0
Percent Identity: 100.000
  Percent Identity:
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alignment_block:
US-09-528-682-1 x US-10-144-702-194/rev
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Quality:
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; OTHER INFORMATION: n equals a,t,g,
US-10-144-702-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-144-702-194
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US-09-528-682-1 x US-10-027-632-89413
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                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-721-544-2302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                    Sequence 2302, Application US/09721544 GENERAL INFORMATION:
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                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/144,702
CURRENT FILLING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: 09/758,460
PRIOR FILING DATE: 2001-01-11
                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/180,628 PRIOR FILING DATE: 2000-02-04 NUMBER OF SEQ ID NOS: 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PM010C1N
                                                                 APPLICANT:
                                                                                                                         APPLICANT: Arterburn, Matthew APPLICANT: Asghari, Vida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/179,065 PRIOR FILING DATE: 2000-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
      APPLICANT
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LOCATION: (456)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature 
LOCATION: (395)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                              99 ACTTCCCTGAGCCTCAGGTCC 79
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                                                                                                                                                                                                                                                                                                                                     62 ThrSerLeuSerLeuArgSer 68
Drmanac, Radoje
Engleman, Carrie
Faulkner, Brandy
                                                                 Drake, Jim
                                                                                  Damavandi, Simin
Dickson, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity:
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; 0
; 100.000
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                                                                                                                                                                                                                                                                                                                                                                                from: 1
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Length: 7
Gaps: 0
Percent Identity: 100.000

from: سر

ţo:

471

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; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-704-302A-158
                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
    Sequence 158, Application US/09704302A
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA; Homo sapiens US-09-721-544-2302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-704-302A-158
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 158
LENGTH: 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version SEQ ID NO 2302
LENGTH: 470
                                                                                                                                                                                                             APPLICANT: Nieuwenhuizen, Nicolaas
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c1U
CURRENT APPLICATION NUMBER: US/09/704,302A
CURRENT FILING DATE: 2002-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVel Nucleic Acid Sequences Obtained TITLE OF INVENTION: From a cDNA Library of Fetal Liver-Sp FILE REFERENCE: 728CIP CURRENT APPLICATION NUMBER: US/09/721,544 CURRENT FILING DATE: 2000-11-21 PRIOR APPLICATION NUMBER: 09/515,128 PRIOR APPLICATION NUMBER: 09/515,128 PRIOR FILING DATE: 1998-02-13 PRIOR FILING DATE: 1998-02-13
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Strabala, Timothy APPLICANT: Nieuwenhuizen, N
                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 1402
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Tkach, Joe
Tran, Lien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones, Lee
Kita, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang, Fei
Yim, Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palencia, Servando
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Nguyen, Phuong
Nogra, Margie
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Gaps: 0
Percent Identity: 100.000
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; Sequence 86877, Applic:
; GENERAL INFORMATION:
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US-09-528-682-1 x US-10-002-623-355/rev
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; ORGANISM: Homo Sapiens
US-10-002-623-355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-86877
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Ratio: 1.000
Percent Similarity: 100.000
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 355
LENGTH: 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 355, Application US/10002623 GENERAL INFORMATION:
                                                                                                                                                                                                             APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FAPPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OEENER, PETER J.
APPLICANT: UNDERHILL, PETER A.
APPLICANT: UNDERHILL, PETER A.
TITLE OF INVENTION: A METHOD FOR DETERMINING GENETIC
TITLE OF INVENTION: AFFILIATION, SUBSTRUCTURE AND GE
TITLE OF INVENTION: POPULATIONS
FILE REFERENCE: STAN-212
CURRENT APPLICATION NUMBER: US/10/002,623
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: US 60/245,355
PRIOR FILING DATE: 2000-11-01
                                            PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                            PRIOR FILING DATE: 2000-07-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 GluGlnGluValSerAlaLeu 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 GAGCAGGAGGTCTCAGCTCTA
APPLICATION NUMBER: US 60/167,363 FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to reverse of: US-10-002-623-355
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303

Nucleotide

Percent Identity:

Length:

AND GENE FLOW WITHIN HUMAN

: 7 : 0 : 100.000

from: 1

to: 478

alignment_scores

APPLICATION

NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720

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alignment_block:
us-09-528-682-1 x us-10-027-632-86878
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Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-86878
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US-09-528-682-1 x US-10-027-632-86877
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US-10-027-632-86877
                                                                                                                                                                                                                                                            alignment_scores:
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                                                                                                                                                                                        Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 86878, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827,129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ
SEQ ID NO 86878
LENGTH: 478
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SEQ ID NO 86877
LENCTH: 478
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-08-09
                    144 GluTyrArgAspArgTyrTyr 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 GAATATAGAGACAGGTATTAT 244
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224 GAATATAGAGACAGGTATTAT 244
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                                                                                                                                                                                            Percent
                                                                                                                                                                                          Identity:
                                                                                                                                                                                                               Length:
Gaps:
                                                                                    from: 1
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; TYPE: DNA; ORGANISM: HOMO Sapiens; FEATURE: HOMO Sapiens; FEATURE: MISC_feature; LOCATION: (1)...(488); OTHER INFORMATION: n = AUS-09-721-544-3385
seq_documentation_block:
; Sequence 68521, Application US/10027632
                                                                                                                                                                                                    alignment_block:
US-09-528-682-1 x US-09-721-544-3385/rev
                                                      seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-68521
                                                                                                                                                                                                                                                                                                           alignment_scores:
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                                                                                                                                                                                                                                                     Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
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PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 09/034,341
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 24489
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 3385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/721,544
CURRENT FILING DATE: 2000-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained TITLE OF INVENTION: From a cDNA Library of Fetal Liver-Spleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Arterburn, Matthew APPLICANT: Asghari, Vida
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                                                                                                         62 ThrSerLeuSerLeuArgSer 68
                                                                                            ACATCATTAAGCCTTCGAAGT 245
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Lomelli, Michelle
Nguyen, Phuong
Nogra, Margie
Palencia, Servando
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Jones, Lee
Kita, David
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Yim, Kenneth
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Drake, Jim
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Giedt, Gretchen
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Faulkner, Brandy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Labat, Ivan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Veronica
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0
100.000
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alignment_block:
US-09-528-682-1 x US-10-027-632-68521/rev
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                                                                                     PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PPLICATION NUMBER: US 60/198,676
PRIOR PLICING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PPLICATION NUMBER: US 60/185,218
PRIOR PPLICATION NUMBER: US 60/167,363
PRIOR PPLICATION NUMBER: US 60/167,363
PRIOR PPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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; Sequence 295156, Application US/10027632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-295156
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Ratio: 1.000
Percent Similarity: 100.000
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PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23
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SEQ ID NO 68521
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 295156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
FILE REFERENCE: 108827.129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 ACTATCTATTTAAGAGAGTAC 383
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Gaps: 0
Percent Identity: 100.000
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seq_documentation_block:
    Sequence 298567, Application US/10027632
    GENERAL INFORMATION:
    APPLICANT: Wang, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Human US-10-027-632-295156
                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-528-682-1 x US-10-027-632-60190/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Human US-10-027-632-60190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
                                                                                                                    seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-298567
                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-60190
                                                                                                                                                                                                                                                                                                                                                                                Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: US-10-027-632-295156
                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: US-10-027-632-60190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 60190
LENGTH: 502
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 60190, Application US/10027632 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/167, 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE:
                                                                                                                                                                   485 GGGTATGTTTCTACTTCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403 ACTATCTATTTAAGAGAGTAC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 ThrIleTyrLeuArgGluTyr 214
                                                                                                                                                                                                               58 GlyTyrValSerThrSerLeu 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1999-09-28
APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1999-08-09
                                                                                                                                                                     465
                                                                                                                                                                                                                                                                                                                                                                         Length: 7
Gaps: 0
Percent Identity: 100.000
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Gaps:
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FITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129

CURRENT REFERENCE: 108827.129

CURRENT REFILCATION NUMBER: US/10/027,632

CURRENT REFLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-07-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23 60/186,358
PRIOR
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